

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2005, 03:22:53 ; Search time 165 Seconds
(without alignments)
288.312 Million cell updates/sec

Title: US-10-776-989-9

Perfect score: 624

Sequence: 1 RAELTSDKDKMYLNDSSIE.....DPAEDTNYTEKHSLSLFLK 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003Bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	123	2 AAR66806	Aar66806 Extracell
2	597	95.7	201	7 ADES8079	Ades8079 Human Pro
3	597	95.7	340	3 AAY84360	Aay84360 Amino aci
4	597	95.7	397	8 ADP24485	Adp24485 PRO polyp
5	593	95.0	201	7 ABR62858	Abr62858 Human syn
6	589	94.4	201	4 AAM93212	Aam93212 Human pol
7	589	94.4	201	8 ADL30579	Adl30579 Human pro
8	445.5	71.4	202	7 ABR62856	Abr62856 Mouse syn
9	427	68.4	201	7 ABR62857	Abr62857 Rat synde
10	427	68.4	201	7 ADES8077	Ades8077 Rat Prote
11	204	32.7	40	2 AAR66805	Aar66805 Fragment
12	187.5	30.0	190	7 ABR62859	Abr62859 Xenopus s
13	180	28.8	369	4 ABG071159	Abg071159 Novel hum
14	153	24.5	52	5 ABP05027	Abp05027 Human ORF
15	132.5	21.2	208	7 ABR62855	Abr62855 Zebrafish
16	102.5	16.4	676	4 ABB62247	Abb62247 Drosophil
17	92.5	14.8	795	4 ABB61567	Abb61567 Drosophil
18	91.5	14.7	826	3 AAG38474	Aag38474 Arabidops
19	91.5	14.7	885	3 AAG38473	Aag38473 Arabidops
20	91.5	14.7	888	3 AAG38472	Aag38472 Arabidops
21	90	14.4	543	6 ADB10596	Adb10596 Alloiococ
22	90	14.4	568	6 ADB10594	Adb10594 Alloiococ
23	90	14.4	571	6 ADB10592	Adb10592 Alloiococ
24	88.5	14.2	1416	2 AAR67358	Aar67358 Human ast
25	87	13.9	288	8 ADN24238	Adn24238 Bacterial

ALIGNMENTS

RESULT 1

AAR66806

ID AAR66806 standard; peptide; 123 AA.

XX AAR66806;

XX 25-MAR-2003 (revised)

DT 11-SEP-1995 (first entry)

XX Extracellular domain of the mouse syndecan-2 protein.

XX Cell surface; proteoglycan; syndecan; mouse; mammary; epithelial cell;

KW ectodomain; NMuMG; glycosylation; heparan sulphate; chondroitin sulphate;

KW glycosaminoglycan; chimera; chimaeric molecule; effector molecule;

KW receptor; drug; antibody; diagnostic agent.

XX Mus musculus.

XX WO9500633-A2.

PN 05-JAN-1995.

XX 17-JUN-1994; 94WO-US006920.

XX 17-JUN-1993; 93US-00078683.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX Saunders S, Bernfield M, Kato M;

PI WPI; 1995-052071/07.

XX DNA and protein sequences for recombinant syndecan-derived

PT proteoglycan(s) - comprising a core protein having glycosylation sites

PT for heparin sulphate glycosaminoglycan side chains.

XX Claim 22; Page 83; 97pp; English.

XX Peptides AAR66803-810 correspond to the extracellular domains of the

CC mouse syndecans 1-4 or fragments of these domains. The sequence given

CC here represents a 123 amino acid fragment covering the entire

CC extracellular domain of the mouse syndecan-2 protein. The peptides

CC presented all contain a heparan sulphate glycosaminoglycan attachment

CC site (see AAR66794). The functional domains, esp. the soluble

CC extracellular or heparan binding site, of the syndecan molecules (see

CC AAR66797-812 and AAR66818) can be used to construct chimaeras by linking

CC them to biological effector molecules, cell surface receptors, drugs,

26	87	13.9	449	4 ABB66171	Abb66171 Drosophil
27	87	13.9	2237	5 ABB66171	Abb66171 Drosophil
28	87	13.9	2703	4 ABB660074	Abb660074 Drosophil
29	86.5	13.9	399	4 ABB64560	Abb64560 Drosophil
30	86.5	13.9	651	6 ABB64560	Abb64560 Drosophil
31	86.5	13.9	664	6 ABB64560	Abb64560 Drosophil
32	86.5	13.9	700	2 ABB64560	Abb64560 Drosophil
33	86.5	13.9	701	5 ABB64560	Abb64560 Drosophil
34	86.5	13.9	716	2 ABB64560	Abb64560 Drosophil
35	86	13.8	823	4 ABB61359	Abb61359 Drosophil
36	86	13.8	1033	4 ABB61359	Abb61359 Drosophil
37	85.5	13.7	832	4 ABB62517	Abb62517 Human pro
38	85.5	13.7	832	8 ABB62517	Abb62517 Human pro
39	85.5	13.7	832	8 ABB62517	Abb62517 Human pro
40	85.5	13.7	832	8 ABB62517	Abb62517 Human pro
41	85	13.6	1637	6 ABB61359	Abb61359 Drosophil
42	84.5	13.5	1141	6 ABB61359	Abb61359 Drosophil
43	84	13.5	286	4 ABB64418	Abb64418 Drosophil
44	84	13.5	428	5 ABB64418	Abb64418 Drosophil
45	84	13.5	776	3 ABB64418	Abb64418 Drosophil

CC antibodies, diagnostic agents or components of microorganisms. (Updated
CC on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 123 AA;
Query Match 100.0%; Score 624; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.9e-53;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RAE L T S D K D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T T R P L P K I L 60
DB 1 RAE L T S D K D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T T R P L P K I L 60
QY 61 L T S A A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D S 120
DB 61 L T S A A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D S 120
QY 121 L F K 123
DB 121 L F K 123
RESULT 2
ADE58079
ID ADE58079 standard; protein; 201 AA.
XX
AC ADE58079;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P34741, SEQ ID NO 3948.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Belfort K, Costigan M;
XX
XX WPI; 2003-268312/26.
DR GENBANK; P34741.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 201 AA;
Query Match 95.7%; Score 597; DB 7; Length 201;
Best Local Similarity 97.6%; Pred. No. 1.7e-50;
Matches 120; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 1 RAE L T S D K D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T T R P L P K I L 60
DB 21 RAE L T S - - D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T T R P L P K I L 78
QY 61 L T S A A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D S 120
DB 79 L T S A A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D S 138
QY 121 L F K 123
DB 139 L F K 141
RESULT 3
AA84360
ID AA84360 standard; protein; 340 AA.
XX
AC AA84360;
XX
DT 12-JUL-2000 (first entry)
XX
DE Amino acid sequence of the extracellular domain of syndecan-2.
XX
KW Syndecan-2; proteoglycan; syndecan-4; angiogenesis.
XX
OS Homo sapiens.
XX
PN WO200014103-A1.
XX
PD 16-MAR-2000.
XX
PF 18-AUG-1999; 99WO-US018865.
XX
PR 02-SEP-1998; 98US-00145916.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Simons M, Volk R, Horowitz A;
XX
XX WPI; 2000-256934/22.
DR N-PSDB; AA299652.
XX
PT Nucleic acids and vectors useful for the stimulation of angiogenesis in
XX endothelial cells via enhanced expression of syndecan-4.
XX
PS Disclosure; Fig 3; 72pp; English.
XX
XX The present sequence represents for the extracellular domain of syndecan-
CC 2. Syndecans are proteoglycans. The nucleic acid sequence is used to
CC construct the nucleic acids of the invention. These nucleic acids
CC comprise sequences coding for an extracellular domain (chosen from

CC AAZ99651-55), a transmembrane domain (chosen from AAZ99656-61), and the
CC cytoplasmic domain of syndecan-4 protein. The specification describes
CC nucleic acids which are used for the stimulation of angiogenesis via
CC enhanced endothelial expression of syndecan-4 core proteins. The nucleic
CC acids are used to stimulate angiogenesis in myocardium, lung, brain,
CC kidney spleen, liver and/or gastrointestinal tissues
XX
SQ Sequence 340 AA;

Query Match 95.7%; Score 597; DB 3; Length 340;
Best Local Similarity 97.6%; Pred. No. 3.3e-50;
Matches 120; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 RAE L T S D K D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 60
D b 217 R A E L T S - - D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 274
QY 61 L T S A A P K V E T T L N I Q N K I P A O T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D S 120
D b 275 L T S A A P K V E T T L N I Q N K I P A O T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D S 334
QY 121 L F K 123
D b 335 L F K 337

RESULT 4
ADP24485
ID ADP24485 standard; protein; 397 AA.
AC ADP24485;
XX
XX 18-NOV-2004 (first entry)
XX
XX PRO polypeptide SEQ ID NO:1663.
DE
DE PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX
XX Unidentified..
XX
XX WO2004041170-A2.
XX
XX 21-MAY-2004.
XX
XX 30-OCT-2003; 2003WO-US034312.
XX
XX 01-NOV-2002; 2002US-0423394P.
XX
XX (GETH) GENENTECH INC.
XX
XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;

XX
XX WPI; 2004-419628/39.
DR N-PSDB; ADP24484.
XX
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
XX Claim 7; SEQ ID NO 1663; 2940pp; English.
PS
PS The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as

CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.
XX
SQ Sequence 397 AA;

Query Match 95.7%; Score 597; DB 8; Length 397;
Best Local Similarity 97.6%; Pred. No. 4e-50;
Matches 120; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 1 RAE L T S D K D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 60
D b 217 R A E L T S - - D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 274
QY 61 L T S A A P K V E T T L N I Q N K I P A O T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D S 120
D b 275 L T S A A P K V E T T L N I Q N K I P A O T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D S 334
QY 121 L F K 123
D b 335 L F K 337

RESULT 5
ABR62858
ID ABR62858 standard; protein; 201 AA.
XX
AC ABR62858;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human syndecan-2 polypeptide.
DE
XX Syndecan-2; human; angiogenesis.
KW
XX Homo sapiens.
OS
XX WO2003062386-A2.
PN
XX 31-JUL-2003.
PD
XX 17-JAN-2003; 2003WO-US001637.
PF
XX 18-JAN-2002; 2002US-0349939P.
PR
XX (MINU) UNIV MINNESOTA.
PA
XX Ekker SC, Chen EY;
PI
XX WPI; 2003-627457/59.
DR
XX New syndecan-2 antisense polynucleotide, useful for modulating
PT angiogenesis and vasculogenesis in diseases such as rheumatoid arthritis,
PT atherosclerosis, diabetes mellitus, retinopathies, psoriasis and cancer.
XX
XX Example 1; Fig 3; 51pp; English.
PS
XX

CC The present sequence is the protein sequence of human syndecan-2. The
 CC sequence shows 48% identity to that of a newly identified zebrafish
 CC syndecan-2 homologue (see ABR62855), designated EC2. EC2 was shown to be
 CC involved in vasculogenesis and angiogenesis. The invention provides
 CC methods related to modulating syndecan levels and angiogenesis in an
 CC animal, especially using claimed antisense polynucleotides that decrease
 CC expression of a nucleic acid encoding syndecan-2. Also provided are cells
 CC and teleost embryos comprising such antisense polynucleotides, expression
 CC vectors, and methods for identifying syndecan-2-modulating agents, for
 CC identifying an angiogenesis-modulating agent, for promoting angiogenesis
 CC in a vertebrate by administering syndecan-2 or a nucleic acid encoding
 CC it, for reducing angiogenesis by administering the antisense
 CC polynucleotide, and for detecting syndecan-2 expression in a tissue,
 CC especially a tumour tissue. Diseases that can be treated include
 CC rheumatoid arthritis, atherosclerosis, diabetes mellitus, retinopathy,
 CC psoriasis, retrolental fibroplasias and cancer
 XX
 SQ Sequence 201 AA;

Query Match 95.0%; Score 593; DB 7; Length 201;
 Best Local Similarity 96.7%; Pred. No. 4.1e-50;
 Matches 119; Conservative 2; Mismatches 0; Indels 2; Gaps 1;
 QY 1 RAE L T S D K D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 60
 D b 21 R A E L T S - - D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 78
 QY 61 L T S A P K V E T T L N I O N K I P A O T K S P E E T D K E K V L S D S E R K M D P A E D T N V Y T E K H S D S 120
 D b 79 L T S A P K V E T T L N I O N K I P A O T K S P E E T D K E K V L S D S E R K M D P A E D T N V Y T E K H S D S 138
 QY 121 L F K 123
 D b 139 L F K 141

RESULT 6
 AAM93212
 ID AAM93212 standard; protein; 201 AA.
 AC AAM93212;
 XX
 XX 06-NOV-2001 (first entry)
 DT Human polypeptide, SEQ ID NO: 2612.
 DE Human, full length cDNA; cDNA synthesis; oligo-capping.
 XX
 XX Homo sapiens.
 OS
 PN EP1130094-A2.
 XX
 PD 05-SEP-2001.
 XX
 XX 07-JUL-2000; 2000EP-00114089.
 PF
 PR 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-00118774.
 PR 02-MAY-2000; 2000JP-00183765.
 XX
 XX (HELI-) HELIX RES INST.
 PA
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 DR WPI; 2001-524255/58.
 DR N-PSDB; AAK94121.
 XX
 XX 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 PT
 XX Claim 8; SEQ ID NO 2612; 1380pp + Sequence Listing; English.
 PS
 XX

CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesizing the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in CD-ROM
 CC format directly from EPO
 XX
 SQ Sequence 201 AA;

Query Match 94.4%; Score 589; DB 4; Length 201;
 Best Local Similarity 95.9%; Pred. No. 1e-49;
 Matches 118; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
 QY 1 RAE L T S D K D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 60
 D b 21 R A E L T S - - D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 78
 QY 61 L T S A P K V E T T L N I O N K I P A O T K S P E E T D K E K V L S D S E R K M D P A E D T N V Y T E K H S D S 120
 D b 79 L T S A P K V E T T L N I O N K I P A O T K S P E E T D K E K V L S D S E R K M D P A E D T N V Y T E K H S D S 138
 QY 121 L F K 123
 D b 139 L F K 141

RESULT 7
 ADL30579
 ID ADL30579 standard; protein; 201 AA.
 AC ADL30579;
 XX
 XX 20-MAY-2004 (first entry)
 DT Human protein encoded by a full length cDNA clone SeqID 2612.
 DE Human; medicine; signal transduction; glycoprotein; transcription;
 XX oligo-capping method.
 KW Homo sapiens.
 OS
 PN EP1396543-A2.
 XX
 PD 10-MAR-2004.
 XX
 XX 07-JUL-2000; 2003EP-00025638.
 PF
 PR 08-JUL-1999; 99JP-00194486.
 PR 11-JAN-2000; 2000JP-00118774.
 PR 02-MAY-2000; 2000JP-00183865.
 PR 07-JUL-2000; 2000EP-00114089.
 XX
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 PA
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 DR WPI; 2004-204755/20.
 DR N-PSDB; ADL30578.
 XX
 XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full
 PT length human cDNAs.
 PT
 XX Example 1; SEQ ID NO 2612; 1340pp; English.
 PS
 XX This invention relates to a novel primers useful for synthesising full
 CC length cDNA molecules that encode human proteins. Specifically, it refers

CC to secretory or membrane proteins that are potential therapeutic agents/
 CC target molecules in the field of medicine, and in particular genes
 CC encoding proteins that are associated with signal transduction,
 CC glycoproteins and transcription. The present invention describes a method
 CC for efficiently cloning a full length human cDNA from both the 5' and 3'
 CC ends using the oligo-capping method. This polypeptide sequence is a full
 CC length human protein of the invention.

XX Sequence 201 AA;
 Query Match 94.4%; Score 589; DB 8; Length 201;
 Best Local Similarity 95.9%; Pred. No. 1e-49;
 Matches 118; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
 QY 1 RAELTSDKDKMYLNDSSIEEASGVYPIDDDYASASGSGADEVSPELTTTRPLPKIL 60
 DB 21 RAELTS--DKMYLNDSSIEEASGVYPIDDDYASASGSGTDEVSPELTTSRPLPKIL 78
 QY 61 LTSAPKVVETTLNIQNKIPAQTKSPETDKEKVNLSDSERKMDPAEDTNNVTEKHS 120
 DB 79 LTSAPKVVETTLNIQNKIPAQTKSPETDKEKVNLSDSERKMDPAEDTNNVTEKHS 138
 QY 121 LFK 123
 DB 139 LFK 141

RESULT 8
 ABR62856
 ID ABR62856 standard; protein; 202 AA.
 XX
 AC ABR62856;
 DT 04-DEC-2003 (first entry)
 DE Mouse syndecan-2 polypeptide.
 XX Syndecan-2; mouse; angiogenesis.
 OS Mus sp.
 PN WO2003062386-A2.
 PD 31-JUL-2003.
 PF 17-JAN-2003; 2003WO-US0001637.
 XX 18-JAN-2002; 2002US-0349939P.
 PR (MINU) UNIV MINNESOTA.
 PA Ekker SC, Chen EY;
 PI WPI; 2003-627457/59.
 DR New syndecan-2 antisense polynucleotide, useful for modulating
 PT angiogenesis and vasculogenesis in diseases such as rheumatoid arthritis,
 PT atherosclerosis, diabetes mellitus, retinopathies, psoriasis and cancer.
 XX Example 1; Fig 3; 51pp; English.

XX The present sequence is the protein sequence of mouse syndecan-2. The
 CC sequence shows 50% identity to that of a newly identified zebrafish
 CC syndecan-2 homologue (see ABR62855), designated EC2. EC2 was shown to be
 CC involved in vasculogenesis and angiogenesis. The invention provides
 CC methods related to modulating syndecan levels and angiogenesis in an
 CC animal, especially using claimed antisense polynucleotides that decrease
 CC expression of a nucleic acid encoding syndecan-2. Also provided are cells
 CC and telost embryos comprising such antisense polynucleotides, expression
 CC vectors, and methods for identifying syndecan-2-modulating agents, for
 CC identifying an angiogenesis-modulating agent, for promoting angiogenesis
 CC in a vertebrate by administering syndecan-2 or a nucleic acid encoding
 CC it, for reducing angiogenesis by administering the antisense

CC polynucleotide, and for detecting syndecan-2 expression in a tissue,
 CC especially a tumour tissue. Diseases that can be treated include
 CC rheumatoid arthritis, atherosclerosis, diabetes mellitus, retinopathy,
 CC psoriasis, retrolental fibroplasias and cancer
 XX Sequence 202 AA;
 Query Match 71.4%; Score 445.5; DB 7; Length 202;
 Best Local Similarity 72.6%; Pred. No. 1.4e-35;
 Matches 90; Conservative 18; Mismatches 13; Indels 3; Gaps 2;

QY 1 RAELTSDKDKMYLNDSSIEEASGVYPIDDDYASASGSGADEVSPELTTTRPLPKIL 60
 DB 21 RELTS--DKMYLNDSSIEEASGVYPIDDDYSSASGSGADEIESPVLTTSQILPRIP 78
 QY 61 LTSAPKVVETTLNIQNKIPAQTKSPETDKEKVNLSDSERKMDPAEDTNNVTEKHS 119
 DB 79 LTSAPKVVETTLNIQNKIPAQTKSPETDKEEVDISEAEKLGPAIKSTDVYTEKHS 138
 QY 120 LFK 123
 DB 139 NLFK 142

RESULT 9
 ABR62857
 ID ABR62857 standard; protein; 201 AA.
 XX
 AC ABR62857;
 DT 04-DEC-2003 (first entry)
 DE Rat syndecan-2 polypeptide.
 XX Syndecan-2; rat; angiogenesis.
 OS Rattus sp.
 PN WO2003062386-A2.
 PD 31-JUL-2003.
 PF 17-JAN-2003; 2003WO-US0001637.
 XX 18-JAN-2002; 2002US-0349939P.
 PR (MINU) UNIV MINNESOTA.
 PA Ekker SC, Chen EY;
 PI WPI; 2003-627457/59.
 DR New syndecan-2 antisense polynucleotide, useful for modulating
 PT angiogenesis and vasculogenesis in diseases such as rheumatoid arthritis,
 PT atherosclerosis, diabetes mellitus, retinopathies, psoriasis and cancer.
 XX Example 1; Fig 3; 51pp; English.

XX The present sequence is the protein sequence of rat syndecan-2. The
 CC sequence shows homology to a newly identified zebrafish syndecan-2
 CC homologue (see ABR62855), designated EC2. EC2 was shown to be involved in
 CC vasculogenesis and angiogenesis. The invention provides methods related
 CC to modulating syndecan levels and angiogenesis in an animal, especially
 CC using claimed antisense polynucleotides that decrease expression of a
 CC nucleic acid encoding syndecan-2. Also provided are cells and telost
 CC embryos comprising such antisense polynucleotides, expression vectors,
 CC and methods for identifying syndecan-2-modulating agents, for identifying
 CC an angiogenesis-modulating agent, for promoting angiogenesis in a
 CC vertebrate by administering syndecan-2 or a nucleic acid encoding it, for
 CC reducing angiogenesis by administering the antisense polynucleotide, and
 CC for detecting syndecan-2 expression in a tissue, especially a tumour
 CC tissue. Diseases that can be treated include rheumatoid arthritis,
 CC atherosclerosis, diabetes mellitus, retinopathy, psoriasis, retrolental

CC fibroplasias and cancer
 XX Sequence 201 AA;
 SQ

Query Match 68.4%; Score 427; DB 7; Length 201;
 Best Local Similarity 69.1%; Pred. No. 8.9e-34;
 Matches 85; Conservative 19; Mismatches 17; Indels 2; Gaps 1;

QY 1 RAELESDKDKMYLNSIEEASGVYPIDDDDYASAGSGADEVDVESPELTTRPLPKIL 60
 DB 21 RAELETS--DKMYLSSSIEEASGLYPIDDDYSSAGSGAYEDKGSPLTTSQILPRIS 78
 QY 61 LSAAPKVVETTLNIQNKIPAQTKSPETDKKYNLSDSERKMDPAEDTNNVTEKHSDS 120
 DB 79 LSAAPEVETMTLKTQSITPTQTESPEETDKKEFEISEAEKQDPAVKSTDVYTEKHSN 138

QY 121 LFK 123
 DB 139 LFK 141

RESULT 10
 ADE58077
 ID ADE58077 standard; protein; 201 AA.
 XX
 AC ADE58077;
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein P34900, SEQ ID NO 3946.
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX Rattus norvegicus.
 OS
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX
 XX WPI; 2003-268312/26.
 DR GENBANK; P34900.
 XX
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 201 AA;

Query Match 68.4%; Score 427; DB 7; Length 201;
 Best Local Similarity 69.1%; Pred. No. 8.9e-34;
 Matches 85; Conservative 19; Mismatches 17; Indels 2; Gaps 1;

QY 1 RAELESDKDKMYLNSIEEASGVYPIDDDDYASAGSGADEVDVESPELTTRPLPKIL 60
 DB 21 RAELETS--DKMYLSSSIEEASGLYPIDDDYSSAGSGAYEDKGSPLTTSQILPRIS 78

QY 61 LSAAPKVVETTLNIQNKIPAQTKSPETDKKYNLSDSERKMDPAEDTNNVTEKHSDS 120
 DB 79 LSAAPEVETMTLKTQSITPTQTESPEETDKKEFEISEAEKQDPAVKSTDVYTEKHSN 138

QY 121 LFK 123
 DB 139 LFK 141

RESULT 11
 AAR66805
 ID AAR66805 standard; peptide; 40 AA.
 XX
 AC AAR66805;

XX
 DT 25-MAR-2003 (revised)
 DT 11-SEP-1995 (first entry)

XX Fragment of extracellular domain of the mouse syndecan-2 protein.

XX Cell surface; proteoglycan; syndecan; mouse; mammary; epithelial cell;
 KW ectodomain; NMuMG; glycosylation; heparan sulphate; chondroitin sulphate;
 KW glycosaminoglycan; chimaera; chimaeric molecule; effector molecule;
 KW receptor; drug; antibody; diagnostic agent.

XX Mus musculus.

XX WO9500633-A2.

XX PD 05-JAN-1995.

XX PF 17-JUN-1994; 94WO-US006920.

XX PR 17-JUN-1993; 93US-00078683.

XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX Saunders S, Bernfield M, Kato M;

XX WPI; 1995-052071/07.

XX DNA and protein sequences for recombinant syndecan-derived
 PT proteoglycan(s) - comprising a core protein having glycosylation sites
 PT for heparin sulphate glycosaminoglycan side chains.

XX Claim 22; Page 83; 97pp; English.

XX Peptides AAR66803-810 correspond to the extracellular domains of the

CC mouse syndecans 1-4 or fragments of these domains. The sequence given
 CC here represents a 40 amino acid fragment of the mouse syndecan-2 protein
 CC extracellular domain. The peptides presented all contain a heparan
 CC sulphate glycosaminoglycan attachment site (see AAR66794). The functional
 CC domains, esp. the soluble extracellular or heparan binding site, of the
 CC syndecan molecules (see AAR66797-812 and AAR66818) can be used to
 CC construct chimeras by linking them to biological effector molecules,
 CC cell surface receptors, drugs, antibodies, diagnostic agents or
 CC components of microorganisms. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 XX Sequence 40 AA;

Query Match 32.7%; Score 204; DB 2; Length 40;
 Best Local Similarity 100.0%; Pred. No. 9.7e-13;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RAEITSDKDKMYLDNSSIIEASGVYPIDDDDYASASGSG 40
 DB 1 RAEITSDKDKMYLDNSSIIEASGVYPIDDDDYASASGSG 40

RESULT 12
 ABR62859
 ID ABR62859 standard; protein; 190 AA.
 XX
 AC ABR62859;

DT 04-DEC-2003 (first entry)
 XX
 DE Xenopus syndecan-2 polypeptide.
 XX
 KW Syndecan-2; angiogenesis.

OS Xenopus sp.
 XX
 PN WO2003062386-A2.

PD 31-JUL-2003.
 XX
 PF 17-JAN-2003; 2003WO-US001637.
 XX
 PR 18-JAN-2002; 2002US-034939P.

XX (MINU) UNIV MINNESOTA.
 XX
 PI Ekker SC, Chen EY;
 XX
 DR WPI; 2003-627457/59.

XX New syndecan-2 antisense polynucleotide, useful for modulating
 PT angiogenesis and vasculogenesis in diseases such as rheumatoid arthritis,
 PT atherosclerosis, diabetes mellitus, retinopathies, psoriasis and cancer.

XX Example 1; Fig 3; 51pp; English.

XX The present sequence is the protein sequence of Xenopus syndecan-2. The
 CC sequence shows homology to a newly identified zebrafish syndecan-2
 CC homologue (see ABR62855), designated EC2. EC2 was shown to be involved in
 CC vasculogenesis and angiogenesis. The invention provides methods related
 CC to modulating syndecan levels and angiogenesis in an animal, especially
 CC using claimed antisense polynucleotides that decrease expression of a
 CC nucleic acid encoding syndecan-2. Also provided are cells and teloeost
 CC embryos comprising such antisense polynucleotides, expression vectors,
 CC and methods for identifying syndecan-2-modulating agents, for identifying
 CC an angiogenesis-modulating agent, for promoting angiogenesis in a
 CC vertebrate by administering syndecan-2 or a nucleic acid encoding it, for
 CC reducing angiogenesis by administering the antisense polynucleotide, and
 CC for detecting syndecan-2 expression in a tissue, especially a tumour
 CC tissue. Diseases that can be treated include rheumatoid arthritis,
 CC atherosclerosis, diabetes mellitus, retinopathy, psoriasis, retrolental
 CC fibroplasias and cancer

XX

SQ Sequence 190 AA;

Query Match 30.0%; Score 187.5; DB 7; Length 190;
 Best Local Similarity 37.0%; Pred. No. 3e-10;
 Matches 47; Conservative 23; Mismatches 34; Indels 23; Gaps 6;

QY 3 ELTSDKDKMYLDNSSIIEASGVYPIDDDDYASASGSGA---DEDVESPELTITRPL--- 56
 DB 19 ETWAQADRLYIDST---ESSGNYPVDDDDYSGSGGIPAHDDDDNVDNVLITVQTLISS 75
 QY 57 PKILLTSAAPKVETTTLTNIQKIPAOQTKSPETDKEKVLSDSERKMDPAEEDTN-VYTE 115
 DB 76 P-----SSEMPYVDVTTTLTKTQKWAPEKPEGEVESTNVL-----VHENKNIQTA 122
 QY 116 KHSDSLIF 122
 DB 123 THTENLNF 129

RESULT 13
 ABR607159
 ID ABR607159 standard; protein; 369 AA.
 XX
 AC ABR607159;

DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #7150.

DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.

XX WO200175067-A2.
 XX
 PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.
 XX
 PF 31-MAR-2000; 2000US-00540217.
 XX
 PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS71346.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 20; SEQ ID NO 37518; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity,
 CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 369 AA;

Query Match 28.8%; Score 180; DB 4; Length 369;
 Best Local Similarity 56.4%; Pred. No. 3.9e-09;
 Matches 44; Conservative 2; Mismatches 6; Indels 26; Gaps 3;
 QY 1 RAELESDKDKMYLNSSTEEASGVYPIDDDDYASGSGADEVESPELTTRPLPKIL 60
 DB 55 RAELETS--DKMYLNSSTEEASGVYPIDDDDYASGSGS-----EFMWMKMPK-- 101

QY 61 LTSAPKVTETTLNIONK 78
 DB 102 -----NTQEK 106

RESULT 14
 ABP05027
 ID ABP05027 standard; protein; 52 AA.
 AC ABP05027;
 DT 24-JUN-2002 (first entry)
 DE Human ORFX protein sequence SEQ ID NO:10036.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.

XX Homo sapiens.
 XX WO200192523-A2.
 XX 06-DEC-2001.
 XX 29-MAY-2001; 2001WO-US010836.
 XX 30-MAY-2000; 2000US-0206132P.
 XX 29-AUG-2000; 2000US-0228716P.

XX (CURA-) CURAGEN CORP.
 XX Shinketsu RA, Leach WD;
 XX WPI; 2002-106308/14.
 XX N-PSDB; ABN20779.
 XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders.
 XX Disclosure; SEQ ID NO 10036; 1037pp; English.

XX The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification)). ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,

CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage. N.B. The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 52 AA;

Query Match 24.5%; Score 153; DB 5; Length 52;
 Best Local Similarity 57.7%; Pred. No. 1.4e-07;
 Matches 30; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 62 TSAAPKVTETTLNIONKIPAOIKSPETDKEKVNLSDSERKMDPAEEDTNVY 113
 DB 1 TSAPEVETMLTKQSIPTQTSTESPEETDKGFEISEAEKQDPAVKSTDVY 52

RESULT 15
 ABR62855
 ID ABR62855 standard; protein; 208 AA.

XX ABR62855;
 XX 04-DEC-2003 (first entry)
 XX Zebrafish syndecan-2 polypeptide.

XX Syndecan-2; EC2; zebrafish; angiogenesis; antirheumatic; antiarthritic;
 KW antiarteriosclerotic; antidiabetic; ophthalmological; antipsoriatic;
 KW cytostatic.

OS Brachydanio rerio.
 XX WO2003062386-A2.
 XX 31-JUL-2003.
 XX 17-JAN-2003; 2003WO-US001637.
 XX 18-JAN-2002; 2002US-0349939P.

XX (MINU) UNIV MINNESOTA.
 XX Ekker SC, Chen EY;
 XX WPI; 2003-627457/59.
 XX N-PSDB; ACF79158.

XX New syndecan-2 antisense polynucleotide, useful for modulating
 PT angiogenesis and vasculogenesis in diseases such as rheumatoid arthritis,
 PT atherosclerosis, diabetes mellitus, retinopathies, psoriasis and cancer.

XX Claim 14; Fig 2; 51pp; English.

XX The present sequence is the protein sequence of the zebrafish syndecan-2
 CC homologue. The protein has 48% and 50% sequence identity with human and
 CC mouse syndecan-2, respectively, and is designated EC2 protein. EC2 is
 CC involved in vasculogenesis and angiogenesis. The invention provides
 CC methods related to modulating syndecan levels and angiogenesis in an
 CC animal, especially using claimed antisense polynucleotides that decrease
 CC expression of a nucleic acid encoding syndecan-2. Also provided are cells
 CC and teleost embryos comprising such antisense polynucleotides, expression
 CC vectors, and methods for identifying syndecan-2-modulating agents, for

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2005, 03:36:15 ; Search time 39 Seconds
(without alignments)
303.453 Million cell updates/sec

Title: US-10-776-989-9
Perfect score: 624
Sequence: 1 RAELTSDKDKMYLNSIE.....DPAEDTNYVTEKHSLSLFK 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: piri:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	597	95.7	397	A33880	syndecan 2 - human
2	448.5	71.9	202	I53137	fibroglycan (syndecan-2)
3	427	68.4	211	A42261	heparan sulfate proteoglycan
4	181	29.0	191	S56012	XS-2 protein (homo)
5	93.5	15.0	930	D37271	A-alpha 2 (4) protein
6	92.5	14.8	918	B84580	hypothetical protein
7	91.5	14.7	490	T49096	hypothetical protein
8	89	14.3	181	T24194	hypothetical protein
9	88	14.1	727	T23612	hypothetical protein
10	87.5	14.0	3498	T22330	hypothetical protein
11	87	13.9	288	T22846	hypothetical protein
12	86.5	13.9	395	A54949	syndecan precursor
13	86.5	13.9	611	T06458	nucleolin homolog
14	86.5	13.9	679	S61460	p83/100 protein
15	86.5	13.9	700	G70192	antigen, p83/100 h
16	86	13.8	296	G97799	hypothetical protein
17	86	13.8	644	B71409	hypothetical protein
18	86	13.8	918	T38786	translation initiation factor
19	84.5	13.5	1141	E89824	hypothetical protein
20	84.5	13.5	3488	T34418	hypothetical protein
21	84	13.5	776	A46583	neuroendocrine-specific protein
22	84	13.5	1257	T28937	hypothetical protein
23	83.5	13.4	910	S73361	dnaj homolog protein
24	83	13.3	1659	1 OKBYN2	protein kinase GCN
25	82.5	13.2	308	H86857	highly conserved protein
26	82.5	13.2	817	S53919	hypothetical protein
27	82	13.1	1020	1 QFHUH	neurofilament trip
28	81.5	13.1	783	D86429	F26G16.7 protein
29	81.5	13.1	1166	2 T28680	fibrinogen-binding protein

ALIGNMENTS

RESULT 1

A33880
syndecan 2 - human (fragment)
N:Alternate names: cell surface-associated fibroglycan; heparan sulfate proteoglycan 1
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 05-Nov-1999
R:Accession: A33880
R:Marynen, P.; Zhang, J.; Cassiman, J.J.; Van den Berghe, H.; David, G.
J. Biol. Chem. 264, 7017-7024, 1989
A:Title: Partial primary structure of the 48- and 90-kilodalton core proteins of cell surface and evidence for multiple distinct core proteins at the cell surface of human lung fibroblasts
A:Reference number: A33880; MUID:89214123; PMID:2523388
A:Accession: A33880
A:Molecule type: mRNA
A:Residues: 1-397 <MAR>
A:Cross-references: GB:J04621; NID:gl84428; PIDN:AAA52701.1; PID:G386787
C:Genetics:
A:Gene: GDB:SDC2; HSPG1; HSPG
A:Cross-references: GDB:120065; OMIM:142460
A:Map position: 8q22-q23
C:Keywords: chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmembrane protein
F:341-364/Domain: transmembrane #status predicted <TRM>
F:230/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:237,251,253/Binding site: heparan sulfate (Ser) (covalent) #status predicted

RESULT 2

I53137
fibroglycan (syndecan-2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
R:Accession: I53137
R:David, G.; Bai, X.M.; Van der Schueren, B.; Marynen, P.; Cassiman, J.
Development 119, 841-854, 1993
A:Title: Spatial and temporal changes in the expression of fibroglycan (syndecan-2) during embryonic development
A:Reference number: I53137; MUID:94244478; PMID:8187643

Query Match 14.8%; Score 92.5; DB 2; Length 918;
 Best Local Similarity 19.8%; Pred. No. 5.7;
 Matches 34; Conservative 26; Mismatches 57; Indels 55; Gaps 5;

QY 1 RAELTSDKDKMYLDNNSIEASGVYPIDDDDYASASGSGADEVDS-PEL----- 50
 DB 620 RGNLTSDRSHKFKVDSAGHE---VFPLTEHTDNSRTRESDSDSEFOLGRLGALLAG 676

QY 51 --TTTRPLPKILLTSAAPKVETTLNQNIPAKTQSPEDTKEKVNLS 86
 DB 677 GPRNKXKTLPPYRMSSASSAKAEYI QIDDFGQSSRKDLYSKKASNTETRPSPFPPHSSS 736

QY 87 BETDKE-----KVNLSDSERKMPDAEDTNNYTEKHS 120
 DB 737 DEDDSMQHGRTEKTSLSYSHRVNHDSEELKPTRSSSRIOERSHKPS 788

RESULT 7
 T49096
 hypothetical protein F4F15.280 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C:Accession: T49096
 R:Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Rudd, S.; Lemcke, K.;
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z25015
 A:Accession: T49096
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-490 <ALC>
 A:Cross-references: UNIPROT:Q9SUU8; EMBL:AL049711; GSPDB:GN00061; ATSP:F4F15.280
 A:Experimental source: cultivar Columbia; BAC clone F4F15
 C:Genetics:
 A:Gene: ATSP:F4F15.280
 A:Map position: 3
 A:Introns: 70/2; 433/3

Query Match 14.7%; Score 91.5; DB 2; Length 490;
 Best Local Similarity 24.8%; Pred. No. 3.3;
 Matches 27; Conservative 20; Mismatches 47; Indels 15; Gaps 2;

QY 5 TSDKDKMYLDNNS-----IEASGVYPIDDDDYASASGSGADE-----DVESPE 49
 DB 235 TKPDKRLDYNKDEGFEEELRFMESDGTKPVNNDRVNDAGAAMTKNGLGIDMSAET 294

QY 50 LTTTRPLPKILLTSAAPKVETTLNQNIPAKTQSPEDTKEKVNLS 98
 DB 295 VETFPKSVTSTMDSPDAQPTLNKVCGGKGTETEVADRSTVNHVD 343

RESULT 8
 T24194
 hypothetical protein R11G10.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T24194
 R:Barton, J.
 submitted to the EMBL Data Library, July 1996
 A:Reference number: Z19951
 A:Accession: T24194
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-181 <WIL>
 A:Cross-references: EMBL:Z77668; PIDN:CAB01240.1; GSPDB:GN00023; CESP:R11G10.1
 A:Experimental source: Clone R11G10
 C:Genetics:
 A:Gene: CESP:R11G10.1
 A:Map position: 5
 A:Introns: 44/3

Query Match 14.3%; Score 89; DB 2; Length 181;
 Best Local Similarity 27.1%; Pred. No. 1.6;

Matches 29; Conservative 12; Mismatches 38; Indels 28; Gaps 3;

QY 2 AELTSDKDKMYLDNNSIEASGVYPIDD-----DYASASGSGADEVDSPELT 53
 DB 92 SETPVKHKVHFKNPEPEEIGK---EDDGGAEGEYEEENGSDABEEESPE---- 144

QY 54 RPLPKILLTSAAPKVETTLNQNIPAKTQSPEDTKEKVNLS 100
 DB 145 -----KVEPATSTITTEAQTTTPEEVTDQVSDNIEDDE 178

RESULT 9
 T29612
 hypothetical protein D1014.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T29612
 R:Du, Z.; Leimbac, D.
 submitted to the EMBL Data Library, March 1996
 A:Description: The sequence of C. elegans cosmid D1014.
 A:Reference number: Z20652
 A:Accession: T29612
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-727 <DUZ>
 A:Cross-references: UNIPROT:Q18918; EMBL:U53180; PIDN:AAA96284.1; GSPDB:GN00023; CESP:D1014
 A:Experimental source: strain Bristol N2; clone D1014
 C:Genetics:
 A:Gene: CESP:D1014.5
 A:Map position: 5
 A:Introns: 52/1; 379/2; 442/2; 579/3; 618/2; 647/3; 676/2; 707/3

Query Match 14.1%; Score 88; DB 2; Length 727;
 Best Local Similarity 23.8%; Pred. No. 10;
 Matches 31; Conservative 23; Mismatches 56; Indels 20; Gaps 5;

QY 3 ELTSDKDKMYLDNNSIEASGVYPIDDDDYASASGSGADEVDSPELTTRPLPKILLT 62
 DB 206 ETTTITENK--VADEAPSKAEISIQASQSDHVEKEGESETTTTSDSATTTEK-----KT 258

QY 63 SAAPKVETTLNQNIPAKTQSPEDTKEKVNLS-----SDSERKMDPAEDT-- 110
 DB 259 NGAEVKESETTEKKG-DSSTKSPETVSSVDTTTIERQLKSNNDDEKQVDGNEKESTF 317

QY 111 NVYTEKHS 120
 DB 318 RVLNEDHNEN 327

RESULT 10
 T22330
 hypothetical protein F47A4.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T22330
 R:Northmore, B.
 submitted to the EMBL Data Library, June 1995
 A:Reference number: Z19549
 A:Accession: T22330
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-3498 <WIL>
 A:Cross-references: UNIPROT:Q20497; EMBL:Z49888; PIDN:CAA90064.1; GSPDB:GN00028; CESP:F47A4
 A:Experimental source: clone F47A4
 C:Genetics:
 A:Gene: CESP:F47A4.2
 A:Map position: X
 A:Introns: 36/3; 72/3; 147/2; 228/3; 261/2; 320/2; 847/3; 881/1; 1317/2; 1500/3; 1653/2;

Query Match 14.0%; Score 87.5; DB 2; Length 3498;
 Best Local Similarity 27.2%; Pred. No. 72;
 Matches 34; Conservative 20; Mismatches 64; Indels 7; Gaps 4;

QY 3 ELTSDKDKMYLNSIERASGV-YPIDDDDYASASGGADEVDVSEPLTTRPLPKILL 61
 DB 557 EKNKDEKDEKESVDEHTDLPINPDAAEMADANDKTASERKQLVEEPTGKENE 616
 QY 62 TSAAPK-VETTLNQNKPQATKSPSEETDKE--KYNLSDSERKMD--PAEEDTNVYTE 115
 DB 617 DTSSTAKTSTSAEKSEAPSVDSNDKIDKEPNASSTNDSTKDDTVPMESDPPAATE 676
 QY 116 KHSDS 120
 DB 677 KPES 681

RESULT 11
 T22846
 hypothetical protein F57C7.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T22846
 R:White, S.
 submitted to the EMBL Data Library, February 1996
 A:Reference number: Z19625
 A:Accession: T22846
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-288 <WIL>
 A:Cross-references: UNIPROT:P50605; EMBL:Z69646; PIDN:CAA93474.1; GSPDB:GN00028; CESP:F57C7
 A:Experimental source: clone F57C7
 C:Genetics:
 A:Gene: CESP:F57C7.3
 A:Map position: X
 A:Introns: 51/3; 87/1; 120/3; 191/2; 231/1

Query Match 13.9%; Score 87; DB 2; Length 288;
 Best Local Similarity 29.9%; Pred. No. 4.1;
 Matches 35; Conservative 16; Mismatches 48; Indels 18; Gaps 7;
 QY 17 SIEEASGVYPIDDDDYASASGGADEVDVSEPLTTR----PLPKILLTSAAP-KVETT 71
 DB 64 ADIEVNGSGYPTDDEGDGVHSGS-----KPPSSATTGSKDKVTSPSHAVVTAKPTTVPTT 118
 QY 72 TLNQNKPQATK-SPEETDKE---KYNLSDSERKMDPAEEDTNVTEK--HSDSLF 122
 DB 119 TASF--KPPVQPKPKPAANDKEIKVEEDEDDEDEDDEDEDFADENIHNEEDF 173

RESULT 12
 A54949
 synecan precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A54949
 R:Spring, J.; Paine-Saunders, S.E.; Hynes, R.O.; Bernfield, M.
 Proc. Natl. Acad. Sci. U.S.A. 91, 3334-3338, 1994
 A:Title: Drosophila synecan: conservation of a cell-surface heparan sulfate proteoglycan
 A:Reference number: A54949; MUID:94211858; PMID:8159748
 A:Accession: A54949
 A:Status: preliminary
 A:Molecule type: mRNA; protein
 A:Residues: 1-395 <SPR>
 A:Cross-references: UNIPROT:P49415; GB:U03282; NID:G437282; PIDN:AAC34307.1; PID:G437283
 A:Note: parts of this sequence were confirmed by protein sequencing.
 C:Genetics:
 A:Gene: FlyBase:Scd
 A:Cross-references: FlyBase:FBgn0010415
 C:Keywords: transmembrane protein

Query Match 13.9%; Score 86.5; DB 2; Length 395;
 Best Local Similarity 23.7%; Pred. No. 6.6;
 Matches 41; Conservative 19; Mismatches 48; Indels 65; Gaps 8;
 QY 11 DMVLNNSIEEASGVYPIDDDDYASASGGA-DEEVES----- 47

DB 51 EYIIDDSDIEGSGRGRIHEDLEKOPDY-SGSGFGPDDEADPDQHSNHNTRISQSN 109
 QY 48 -----PELTTRPLPKI-----LLTSAAPKVE-----TTLNQNKI 79
 DB 110 SGINTAHTPTQSSRTPTSTPTPTTAAATQISSFANSSSTTTTTLAPTII 169
 QY 80 PAQTQSP-----BETDKEKVN-----LSDSERKMDPAEEDTNVTEKHS 119
 DB 170 PAEPQQLFPFPDKDLDTSSGDIGADAEDEDDDDKDYDNKELDEID 222

RESULT 13
 T06458
 nucleolin homolog - garden pea
 C:Species: Pisum sativum (garden pea)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T06458
 R:Tong, C.G.; Heieh, H.L.; Blumenthal, S.; Reichler, S.; Balk, J.; Roux, S.J.
 submitted to the EMBL Data Library, August 1995
 A:Description: Molecular cloning and characterization of a cDNA encoding a nucleolin-like
 A:Reference number: Z15692
 A:Accession: T06458
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-611 <TRON>
 A:Cross-references: UNIPROT:Q41042; EMBL:L43510; NID:G940287; PIDN:AAA74208.1; PID:G94028
 A:Experimental source: cv. Alaska
 C:Superfamily: nucleolin; ribonucleoprotein repeat homology

Query Match 13.9%; Score 86.5; DB 2; Length 611;
 Best Local Similarity 26.8%; Pred. No. 11;
 Matches 37; Conservative 23; Mismatches 51; Indels 27; Gaps 5;
 QY 1 RAELTSDKDKMYLNSIERA-----SGVYPIDDDDYASASGGADEVDVSEPLTTR 53
 DB 180 KAASDSDESDR--DSSSDEEAPKAVPAAKAAKKAESSDSSDSESDDEE--DT 235
 QY 54 RPLPKILLTSAAPKVET-----TTLNQNKPQATKSPSEETDKEKYNLSDSER 101
 DB 236 KPTVTAVSKSAVAAKTDEDDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSD 291
 QY 102 KMDPAEEDTNVTEKHS 119
 DB 292 KMNVDKSD 309

RESULT 14
 S61460
 p83/100 protein - Lyme disease spirochete (strain PBre)
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)
 A:Variety: strain PBre
 C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
 C:Accession: S61460
 R:Roessler, D.; Eiffert, H.; Jauris-Heipke, S.; Lehnert, G.; Preac-Mursic, V.; Teepe, J.;
 Med. Microbiol. Immunol. 184, 23-32, 1995
 A:Title: Molecular and immunological characterization of the p83/100 protein of various
 A:Reference number: S61461; MUID:96149106; PMID:8538575
 A:Accession: S61460
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-679 <ROB>
 A:Cross-references: UNIPROT:Q45012; UNIPROT:Q45013
 A:Experimental source: strain PBre
 C:Keywords: surface antigen

Query Match 13.9%; Score 86.5; DB 2; Length 679;
 Best Local Similarity 27.3%; Pred. No. 13;
 Matches 30; Conservative 19; Mismatches 28; Indels 33; Gaps 5;
 QY 6 SDKDK-DMYLNSIEEASGVYPIDDDDYASASGGADEVDVSEPLTTRPLPKILLTSA 64
 DB 218 ADQDKIDELDN--THE-----SDSNITETIEN-----LRDQ 247

QY 65 APKV--ETTTLNQKIPAKTSPETDKEKNVLSDSERKMDPAEDTNV 112
 Db 248 LERATDEEHKKEIESQVDARKKQKELDKRAINLDRKRAQKQKLSAEDNLDV 297

RESULT 15

G70192
 antigen, p83/100 homolog - Lyme disease spirochete
 N;Alternate names: 80K antigen
 C;Species: Borrelia burgdorferi (lyme disease spirochete)
 C;Date: 13-Feb-1998 #sequence revision 13-Feb-1998 #text_change 09-Jul-2004
 C;Accession: G70192; A60332; S61467
 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
 ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A;Authors: Smith, H.O.; Venter, J.C.
 A;Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
 A;Reference number: A70100; MUID:98065943; PMID:9403685
 A;Accession: G70192
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-700 <KLE>
 A;Cross-references: UNIPROT:Q45013; GB:AE001174; GB:AE000783; NID:G2688675; PIDN:AA6709
 A;Experimental source: strain B31
 R;Perng, G.C.; Lerebvre, R.B.; Johnson, R.C.
 Infect. Immun. 59, 2070-2074, 1991
 A;Title: Further characterization of a potent immunogen and the chromosomal gene encoding
 A;Reference number: A60332; MUID:91244453; PMID:2037367
 A;Accession: A60332
 A;Molecule type: DNA
 A;Residues: 1-567, 'S', 569-700 <PER>
 A;Cross-references: GB:M60802
 R;Roessler, D.; Eifert, H.; Jauris-Heipke, S.; Lehnert, G.; Preac-Mursic, V.; Teepe, J.
 Med. Microbiol. Immunol. 184, 23-32, 1995
 A;Title: Molecular and immunological characterization of the p83/100 protein of various
 A;Reference number: S61461; MUID:96149106; PMID:8538575
 A;Accession: S61467
 A;Molecule type: DNA
 A;Residues: 387-470 <ROE>
 A;Cross-references: EMBL:X81514; NID:G928979; PIDN:CAA57234.1; PID:G928980
 A;Experimental source: strain 297
 C;Keywords: surface antigen

Query Match 13.9%; Score 86.5; DB 2; Length 700;
 Best Local Similarity 27.3%; Pred. No. 13;
 Matches 30; Conservative 19; Mismatches 28; Indels 33; Gaps 5;

QY 6 SDKDK-DMYLDNSIEEASGVYFIDDDYASASGSGADEVSPELTTTRPLPKILLTSA 64
 Db 239 ADQDKIDIEDN--IHE-----SDSNITETIEN-----LRDQ 268

QY 65 APKV--ETTTLNQKIPAKTSPETDKEKNVLSDSERKMDPAEDTNV 112
 Db 269 LERATDEEHKKEIESQVDARKKQKELDKRAINLDRKRAQKQKLSAEDNLDV 318

Search completed: March 23, 2005, 04:14:32
 Job time : 42 secs

THIS PAGE BLANK (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2005, 03:29:34 ; Search time 176 Seconds
(without alignments)
357.874 Million cell updates/sec

Title: US-10-776-989-9

Perfect score: 624

Sequence: 1 RAEIISDKDKMYLDNSSIE.....DPAEEDTNYVTEKHSLSLFLK 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	597	95.7	201	1 SDC2 HUMAN	P34741 homo sapien
2	593	95.0	201	2 Q6PI56	Q6PI56 homo sapien
3	448.5	71.9	202	1 SDC2 MOUSE	P43407 mus musculus
4	430.5	69.0	175	2 Q99L05	Q99L05 mus musculus
5	427	68.4	201	1 SDC2 RAT	P34900 rattus norv
6	427	68.4	211	2 Q6IRK3	Q6IRK3 rattus norv
7	383	61.4	201	2 Q8JY0	Q8JY0 gallus gall
8	379	60.7	201	2 Q8JYX9	Q8JYX9 gallus gall
9	379	60.7	201	2 Q76BY7	Q76BY7 gallus gall
10	188	30.1	191	1 SDC2 XENLA	P49414 xenopus lae
11	181	29.0	191	2 Q7L2K2	Q7L2K2 xenopus lae
12	132.5	21.2	208	2 Q902V9	Q902V9 brachydanio
13	132.5	21.2	208	2 Q61666	Q61666 ashbya goss
14	102.5	16.4	440	2 Q75W88	Q75W88 ashbya goss
15	102.5	16.4	634	2 Q6CGJ1	Q6CGJ1 yarrowia li
16	102.5	16.4	676	2 Q9VB94	Q9VB94 drosophila
17	100.5	16.1	657	2 Q17547	Q17547 caenorhabdi
18	100.5	16.1	657	2 Q9TW41	Q9TW41 caenorhabdi
19	97	15.5	1268	2 Q6CGN4	Q6CGN4 yarrowia li
20	96.5	15.5	257	2 Q6BGS9	Q6BGS9 debaryomyce
21	96	15.4	1015	2 Q863P2	Q863P2 dictyosteli
22	93.5	15.0	940	1 MAZA SCHCO	P37938 schizophyll
23	93.5	15.0	1022	2 Q7Q9D9	Q7Q9D9 anopheles g
24	92.5	14.8	918	2 Q82206	Q82206 arabisopsis
25	92.5	14.8	918	2 Q6NQ05	Q6NQ05 arabisopsis
26	92.5	14.8	1271	2 Q9VBK6	Q9VBK6 drosophila
27	92	14.7	702	2 Q7RS81	Q7RS81 plasmodium
28	91.5	14.7	490	2 Q9SU88	Q9SU88 arabisopsis
29	91.5	14.7	499	2 Q8L641	Q8L641 arabisopsis
30	91	14.6	1233	2 Q6BP78	Q6BP78 debaryomyce
31	91	14.6	1405	2 Q8EVL6	Q8EVL6 mycoplasma

RESULT 1

SDC2_HUMAN	SDC2_HUMAN	STANDARD;	PRT;	201 AA.
ID	SDC2_HUMAN	STANDARD;	PRT;	201 AA.
AC	P34741; Q9H6V1;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Syndecan-2 precursor (Fibroglycan) (Heparan sulfate proteoglycan core protein) (HSPG) (SYND2).			
DE	Name=SDC2; Synonyms=HSPG1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung fibroblast;			
RX	MEDLINE=69214123; PubMed=2523388;			
RA	Warynen P., Zhang J., Cassiman J.J., den Berghe H., David G.;			
RT	"Partial primary structure of the 48- and 90-kilodalton core proteins of cell surface-associated heparan sulfate proteoglycans of lung fibroblasts. Prediction of an integral membrane domain and evidence for multiple distinct core proteins at the cell surface of human lung fibroblasts."			
RL	J. Biol. Chem. 264:7017-7024(1989).			
RP	SEQUENCE FROM N.A.			
RX	PubMed=14702039; DOI=10.1038/ngl1285;			
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,			
RA	Wakanatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,			
RA	Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,			
RA	Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,			
RA	Shaharari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,			
RA	Nagahara A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,			
RA	Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,			
RA	Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,			
RA	Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,			
RA	Fujimori K., Tanai H., Kimata M., Watanabe S., Chiba Y.,			
RA	Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hota T.,			
RA	Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,			
RA	Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,			
RA	Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,			
RA	Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,			
RA	Moriya S., Momiya N., Satoh N., Takami Y., Terashima Y., Suzuki O.,			
RA	Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,			
RA	Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,			
RA	Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,			
RA	Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,			
RA	Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,			
RA	Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,			
RA	Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,			
RA	Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,			
RA	Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,			
RA	Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,			

ALIGNMENTS

32	90.5	14.5	221	2	Q84XT6	Q84XT6 phytophthor
33	90	14.4	632	2	Q6NKT4	Q6NKT4 arabidopsis
34	89.5	14.3	580	2	Q724P9	Q724P9 listeria mo
35	89.5	14.3	921	2	Q9IFX3	Q9IFX3 human astro
36	89	14.3	331	2	Q7SYL5	Q7SYL5 brachydanio
37	89	14.3	354	2	Q74256	Q74256 emericella
38	89	14.3	814	2	Q6C247	Q6C247 yarrowia li
39	88.5	14.2	1115	2	Q6C8E7	Q6C8E7 yarrowia li
40	88	14.1	351	2	Q6P130	Q6P130 brachydanio
41	88	14.1	727	2	Q18918	Q18918 caenorhabdi
42	88	14.1	1604	2	Q90662	Q90662 gallus gall
43	87.5	14.0	652	2	Q6CK58	Q6CK58 kluveromyc
44	87.5	14.0	1033	2	Q8D6Y3	Q8D6Y3 vibrio vuln
45	87.5	14.0	1505	2	Q8JKF9	Q8JKF9 heliothis z

RA Okumura K., Negase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RL cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Cell surface proteoglycan that bears heparan sulfate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the syndecan proteoglycan family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J04621; AAAS2701.1; AUT_INIT.
 DR EMBL: AK025488; BAB15150.1; -.
 DR EMBL: BC049836; AAH49836.1; -.
 DR HSSP: P31431; 1EJP.
 DR Genew: HGNC:10659; SDC2.
 DR H-InvDB: HX0007666; -.
 DR MIM: 142460; -.
 DR GO: GO:0005887; C:integral to plasma membrane; NAS.
 DR InterPro: IPR003585; Neuroxin-like.
 DR InterPro: IPR001050; Syndecan.
 DR Pfam: PF01034; Syndecan; 1.
 DR SMART: SM00294; 4.1m; 1.
 DR PROSITE: PS00964; SYNDECAN; 1.
 KW Glycoprotein; Heparan sulfate; Proteoglycan; Signal; Transmembrane.
 FT SIGNAL 1 18 Potential.
 FT CHAIN 19 201 Syndecan-2.
 FT DOMAIN 19 144 Extracellular (Potential).
 FT TRANSMEM 145 169 Potential.
 FT DOMAIN 170 201 Cytoplasmic (Potential).
 FT SITE 142 143 Cleavage of ectodomain (Potential).
 FT CARBOHYD 41 41 O-linked (Xyl. . .) (glycosaminoglycan)
 FT FT O-linked (Xyl. . .) (glycosaminoglycan)
 FT FT O-linked (Xyl. . .) (glycosaminoglycan)
 FT FT O-linked (Xyl. . .) (glycosaminoglycan)
 FT FT O-linked (Xyl. . .) (glycosaminoglycan)
 FT FT T -> S (in Ref. 2).
 FT CONFLICT 71 71 I -> T (in Ref. 2).
 FT CONFLICT 150 150 I -> T (in Ref. 2).
 FT SEQUENCE 201 AA; 22174 MW; 7B7F175650641054 CRC64;
 Query Match 95.7%; Score 597; DB 1; Length 201;
 Best Local Similarity 97.6%; Pred. No. 6.1e-41;

Matches 120; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
 QY 1 RAE L T S D K D K M Y L D N S S I E E A S G V Y P I D D D Y A S A G S G A D E D V E S P E L T T R P L P K I L 60
 DB |||||
 DB 21 RAE L T S - D K D M Y L D N S S I E E A S G V Y P I D D D Y A S A G S G A D E D V E S P E L T T R P L P K I L 78
 QY 61 L T S A A P K V E T T L N T I N Q N K I P A Q T K S P E E T D K S K V N L S D S E R K M D P A E D T N V Y T E K H S D S 120
 DB 79 L T S A A P K V E T T L N T I N Q N K I P A Q T K S P E E T D K S K V N L S D S E R K M D P A E D T N V Y T E K H S D S 138
 QY 121 L F K 123
 DB 139 L F K 141
 RESULT 2
 Q6PIS6 PRELIMINARY; PRT; 201 AA.
 AC Q6PIS6;
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE Syndecan 2.
 GN Name=SDC2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RC Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Cell surface proteoglycan (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to the syndecan proteoglycan family.
 DR EMBL: BC030133; AAH30133.1; -.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0008092; F:cytoskeletal protein binding; IEA.
 DR InterPro: IPR001050; Syndecan.
 DR Pfam: PF01034; Syndecan; 1.
 DR PROSITE: PS00964; SYNDECAN; 1.
 KW Glycoprotein; Heparan sulfate; Proteoglycan; Transmembrane.
 SQ SEQUENCE 201 AA; 22160 MW; 7DA4159D54741054 CRC64;
 Query Match 95.0%; Score 593; DB 2; Length 201;
 Best Local Similarity 96.7%; Pred. No. 1.3e-40;
 Matches 119; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 RAE1TSDKDKMYLDNSSLSEASGVPIDDDDYASAGSGADEVSPSPETLTPRPKIL 60
 DB 21 RAE1TSDKDKMYLDNSSLSEASGVPIDDDDYASAGSGADEVSPSPETLTPRPKIL 78
 QY 61 LTAAPKVTETLTIQNKIPAKTSPEETDKKVNLSDSERKMDPAEDTNNVTEKHS 120
 DB 79 LTAAPKVTETLTIQNKIPAKTSPEETDKKVNLSDSERKMDPAEDTNNVTEKHS 138
 QY 121 LFK 123
 DB 139 LFK 141

RESULT 3

SDC2_MOUSE STANDARD; PRT; 202 AA.
 AC P43407;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Syndecan-2 precursor (fibroglycan) (Heparan sulfate proteoglycan core protein) (HSPG) (SYND2)
 GN Name=Synd2; Synonym=Hspg1, Synd2;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=94244478; PubMed=8187643;
 RA David G.J., Bai X.M., van der Schueren B., Marynen P., Cassiman J.J., van den Bergh H.;
 RT "Spatial and temporal changes in the expression of fibroglycan (syndecan-2) during mouse embryonic development.";
 RL Development 119:841-854 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Niki K., Oosato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schram L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.D., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sanderlin A., Schneider C., Sempile C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -I- FUNCTION: Cell surface proteoglycan that bears heparan sulfate.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -I- TISSUE SPECIFICITY: Preferential expression in cells of mesenchymal origin.
 CC -I- SIMILARITY: Belongs to the syndecan proteoglycan family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U00674; AAA17781.1; -;
 DR EMBL; AK011042; BAB27354.1; -;
 DR EMBL; BC047144; AHA47144.1; -;
 DR PIR; I53137; I53137.
 DR HSSP; P31431; 1EJP.
 DR MGD; MGI:1349165; Sdc2.
 DR InterPro; IPR003585; Neurexin-like.
 DR InterPro; IPR001050; Syndecan.
 DR Pfam; PF01034; Syndecan; 1.
 DR SMART; SM00294; 4.lm; 1.
 DR PROSITE; PS00964; SYNDECAN; 1.
 DR GlycoProtein; Heparan sulfate; Proteoglycan; Signal; Transmembrane.
 FT SIGNAL 1 18 Potential.
 FT CHAIN 19 202 Syndecan-2.
 FT DOMAIN 19 145 Extracellular (Potential).
 FT TRANSMEM 146 170 Potential.
 FT DOMAIN 171 202 Cytoplasmic (Potential).
 FT CARBOHYD 41 41 O-linked (Xyl...) (glycosaminoglycan) (Potential).
 FT CARBOHYD 53 53 O-linked (Xyl...) (glycosaminoglycan) (Potential).
 FT CARBOHYD 55 55 O-linked (Xyl...) (glycosaminoglycan) (Potential).
 FT CARBOHYD 57 57 O-linked (Xyl...) (glycosaminoglycan) (Potential).
 FT SITE 143 144 Cleavage of ectodomain (Potential).
 SQ SEQUENCE 202 AA; 22131 MW; C213D1B64D88376F CRC64;
 Query Match 71.9%; Score 448.5; DB 1; Length 202;
 Best Local Similarity 73.4%; Pred. No. 7.7e-29;
 Matches 91; Conservative 17; Mismatches 13; Indels 3; Gaps 2;
 QY 1 RAE1TSDKDKMYLDNSSLSEASGVPIDDDDYASAGSGADEVSPSPETLTPRPKIL 60
 DB 21 RAE1TSDKDKMYLDNSSLSEASGVPIDDDDYASAGSGADEVSPSPETLTPRPKIL 78
 QY 61 LTAAPKVTETLTIQNKIPAKTSPEETDKKVNLSDSERKMDPAEDTNNVTEKHS 120
 DB 79 LTAAPKVTETLTIQNKIPAKTSPEETDKKVNLSDSERKMDPAEDTNNVTEKHS 138
 QY 121 LFK 123
 DB 139 LFK 141

[illegible]

Db 89 LTSAAPEVETWTLKQSIPTQTSTSPRETDKKEFEISEAEKQDDPAVKSTDVYTEKHSN 142

Qy 121 LFK 123
|||

Db 149 LFK 151

RESULT 7

Q8JIY0 PRELIMINARY; PRT; 201 AA.

ID Q8JIY0

AC Q8JIY0;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Syndecan-2 variant 1.

OS Gallus gallus (Chicken).

OC Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

NCBI_TaxID=9031;

RN NCBI_TaxID=9031;

RP [1]

RA SEQUENCE FROM N.A.

RA Chen L., Couchman J.R., Smith J., Woods A.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Cell surface proteoglycan (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the syndecan proteoglycan family.

DR EMBL; AF508228; AAM28901.1; -.

DR HSP; P31431; IEJP

DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0008092; F: cytoskeletal protein binding; IEA.

DR InterPro; IPR003585; Neurexin-like.

DR InterPro; IPR001050; Syndecan.

DR Pfam; PF01034; Syndecan; 1.

DR SMART; SM00294; 4.lm; 1.

DR PROSITE; PS00964; SYNDECAN; 1.

DR GlycoProtein; Heparan sulfate; Proteoglycan; Transmembrane.

KW

SQ SEQUENCE 201 AA; 22084 MW; BC64EFD2C26C030A CRC64;

Query Match 61.4%; Score 383; DB 2; Length 201;

Best Local Similarity 61.8%; Pred. No. 1.7e-23;

Matches 76; Conservative 23; Mismatches 22; Indels 2; Gaps 1

Qy 1 RAE LTSADKDKOMYLDNLSIEASGVYPIDDDDYASAGSGADEVESPELTTRPLPKIL 60

Db 21 RADLTS -DKDLYLDNLSVEASGVYPIDDDDYSGSGAEDEDSVTVTTSRIVPKLP 78

Qy 61 LTSAAPEVETWTLNQNKIQAQTKSPRETDKKYNLSDSRKMDPAEDTQVYTEKHSN 120

Db 79 TTSASAEATTVMQTMQAQTKSPREIDKEERPEVDSKKKSNPEGDDTQVTEKHSN 138

Qy 121 LFK 123
|||

Db 139 LFK 141

RESULT 8

Q8JIY9 PRELIMINARY; PRT; 201 AA.

ID Q8JIY9

AC Q8JIY9;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Syndecan-2 variant 2.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

NCBI_TaxID=9031;

RN NCBI_TaxID=9031;

RP [1]

RA SEQUENCE FROM N.A.

RA Chen L., Couchman J.R., Smith J., Woods A.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Cell surface proteoglycan (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the syndecan proteoglycan family.
 DR EMBL: AF508229; AAM28902.1; -.
 DR HSSP: P31431; IEJP.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0008092; F: cytoskeletal protein binding; IEA.
 DR InterPro: IPR003585; Neurexin-like.
 DR InterPro: IPR001050; Syndecan.
 DR Pfam: PF01034; Syndecan; 1.
 DR SMART: SM00294; 4.1m; 1.
 DR PROSITE: PS00964; SYNDECAN; 1.
 DR Glycoprotein; Heparan sulfate; Proteoglycan; Transmembrane.
 KW Glycoprotein; Heparan sulfate; Proteoglycan; Transmembrane.
 SQ SEQUENCE 201 AA; 22056 MW; 76AF01C2DC8CE58B CRC64;

Query Match 60.7%; Score 379; DB 2; Length 201;
 Best Local Similarity 61.0%; Pred. No. 3.5e-23;
 Matches 75; Conservative 23; Mismatches 23; Indels 2; Gaps 1;

QY 1 RAE L T S D S A R A E T T T V K M Q T K M P A Q T K S P E E I D K E R P E V D S K K S N E P G D D T D V F T E K H S E N 138
 DB 21 RAD L T S - - D K O L Y L D N S S V E E A S G V P I D D D Y A S A G S G A D E D V S P E L T T R P L P K I L 60
 QY 61 L T S A A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K N L S D S E R K M D P A E E D T N V T T E K H S D S 120
 DB 79 T T S D S A R A E T T T V K M Q T K M P A Q T K S P E E I D K E R P E V D S K K S N E P G D D T D V F T E K H S E N 138
 QY 121 L F K 123
 DB 139 L F Q 141

RESULT 9
 Q76EY7 PRELIMINARY; PRT; 201 AA.
 AC Q76EY7
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Syndecan-2.
 GN Names=SDC2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Yoshizawa K., Inaba K., Mannen H., Kikuchi T., Mizutani M., Tsuji S.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cell surface proteoglycan (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the syndecan proteoglycan family.
 DR EMBL: AB103611; BAD1351.1; -.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0008092; F: cytoskeletal protein binding; IEA.
 DR InterPro: IPR001050; Syndecan.
 DR Pfam: PF01034; Syndecan; 1.
 DR PROSITE: PS00964; SYNDECAN; 1.
 DR Glycoprotein; Heparan sulfate; Proteoglycan; Transmembrane.
 KW Glycoprotein; Heparan sulfate; Proteoglycan; Transmembrane.
 SQ SEQUENCE 201 AA; 22086 MW; 6AD564CB0F5808B CRC64;

Query Match 60.7%; Score 379; DB 2; Length 201;
 Best Local Similarity 61.0%; Pred. No. 3.5e-23;
 Matches 75; Conservative 23; Mismatches 23; Indels 2; Gaps 1;

QY 1 RAE L T S D S A R A E T T T V K M Q T K M P A Q T K S P E E T D K E K N L S D S E R K M D P A E E D T N V T T E K H S D S 120
 DB 21 RAD L T S - - D K O L Y L D N S S V E E A S G V P I D D D Y A S A G S G A D E D V S P E L T T R P L P K I L 60
 QY 61 L T S A A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K N L S D S E R K M D P A E E D T N V T T E K H S D S 120
 DB 79 T T S D S A R A E T T T V K M Q T K M P A Q T K S P E E I D K E R P E V D S K K S N E P G D D T D V F T E K H S E N 138
 QY 121 L F K 123
 DB 139 L F Q 141

Db 79 T T S D S A R A E T T T V K M Q T K M P A Q T K S P E E I D K E R P E V D S K K S N E P G D D T D V F T E K H S E N 138
 QY 121 L F K 123
 Db 139 L F Q 141

RESULT 10
 SDC2_XENLA STANDARD; PRT; 191 AA.
 ID SDC2_XENLA
 AC F49414; O424473;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Syndecan-2 precursor (SYND2) (Xsyn-2).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95344398; PubMed=7619084;
 RA Rosenblum N.D., Botelho B.B., Bernfield M.;
 RT "Expression of a Xenopus counterpart of mammalian syndecan 2 during embryogenesis";
 RL Biochem. J. 309:69-76(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RG NIH - Xenopus Gene Collection (XGC) project;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97109510; PubMed=8951790; DOI=10.1016/0925-4773(96)00584-9;
 RA Teel A.L., Yost H.J.;
 RT "Embryonic expression patterns of Xenopus syndecans";
 RL Mech. Dev. 59:115-127(1996).
 CC -1- FUNCTION: Cell surface proteoglycan that bears heparan sulfate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the syndecan proteoglycan family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
 CC EMBL: U24433; AAA87197.1; -.
 DR EMBL: BC041490; AAH41490.1; -.
 DR EMBL: U41760; AA881325.1; -.
 DR HSSP: F31431; IEJP.
 DR InterPro: IPR003585; Neurexin-like.
 DR InterPro: IPR001050; Syndecan.
 DR Pfam: PF01034; Syndecan; 1.
 DR SMART: SM00294; 4.1m; 1.
 DR PROSITE: PS00964; SYNDECAN; 1.
 KW Glycoprotein; Heparan sulfate; Proteoglycan; Signal; Transmembrane.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 191 Syndecan-2.
 FT DOMAIN 23 137 Extracellular (Potential).
 FT TRANSMEM 138 158 Potential.
 FT DOMAIN 159 191 Cytoplasmic (Potential).
 FT CARBOHYD 36 36 O-linked (Xyl. . .) (glycosaminoglycan) (Potential).
 FT CARBOHYD 48 48 O-linked (Xyl. . .) (glycosaminoglycan) (Potential).
 FT CARBOHYD 50 50 O-linked (Xyl. . .) (glycosaminoglycan) (Potential).
 FT CARBOHYD 52 52 O-linked (Xyl. . .) (glycosaminoglycan) (Potential).
 FT


```
FT CONFLICT 16 16 L -> F (in Ref. 3).
FT CONFLICT 57 58 RG -> HD (in Ref. 3).
FT CONFLICT 63 63 Missing (in Ref. 3).
FT CONFLICT 85 85 E -> D (in Ref. 3).
FT CONFLICT 92 92 Q -> L (in Ref. 1).
FT CONFLICT 114 120 YGKDIV -> HENKII (in Ref. 3).
FT CONFLICT 174 174 R -> G (in Ref. 1).
FT CONFLICT 178 178 S -> R (in Ref. 1).
SQ SEQUENCE 191 AA; 20927 MW; 877A2EBBF396EFCF CRC64;

Query Match
Best Local Similarity 30.1%; Score 188; DB 1; Length 191;
Matches 47; Conservative 23; Mismatches 35; Indels 22; Gaps 5;

QY 3 ELTSDKDKMYLDNSSIEBASGYPIDDDDYASAGSG-----ADEVSEPLTTTRPL-- 56
DB 19 ETWAQADRLYIDST---ESSGNYPVDDDDYSSGSGIPARGDDDENNVLTQTLLS 75
QY 57 -PKILLTSAAPKVETTLNQNIPAKTQSPETDKKYNLSDSRKMDPAEDTNVYTE 115
DB 76 SP-----SSEMPYVETTLTKTQKMAPETKEPGEVESTNTVLVYGKDI-----VQTA 123

QY 116 KHSDSLF 122
DB 124 THTENLF 130

QY 116 KHSDSLF 122
DB 124 THTENLF 130

RESULT 11
Q7L2K2 PRELIMINARY; PRT; 191 AA.
AC Q7L2K2;
DT 01-MAR-2004 (TREMELrel. 26, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DE XS-2 protein (Homolog syndecan 2).
OS Xenopus laevis (African Clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Rosenblum N.D., Botelho B.B., Bernfield M.;
RT "Expression of a Xenopus counterpart of mammalian syndecan 2 during
RL Biochem. J. 309:69-76(1995).
CC -!- FUNCTION: Cell surface proteoglycan (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the syndecan proteoglycan family.
DR PIR; S56012; S56012.
DR HSP; P31431; 1EJP.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR001050; Syndecan.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF01034; Syndecan; 1.
DR PROSITE; PS00430; TONB DEPENDENT REC 1; UNKNOWN 1.
DR PROSITE; PS00430; TONB DEPENDENT REC 1; UNKNOWN 1.
KW Glycoprotein; Heparan sulfate; Proteoglycan; Transmembrane.
SQ SEQUENCE 191 AA; 20981 MW; 05E979B0D7744C1 CRC64;

Query Match
Best Local Similarity 29.0%; Score 181; DB 2; Length 191;
Matches 46; Conservative 23; Mismatches 36; Indels 22; Gaps 5;

QY 3 ELTSDKDKMYLDNSSIEBASGYPIDDDDYASAGSG-----ADEVSEPLTTTRPL-- 56
DB 19 ETWAQADRLYIDST---ESSGNYPVDDDDYSSGSGIPARGDDDENNVLTQTLLS 75
QY 57 -PKILLTSAAPKVETTLNQNIPAKTQSPETDKKYNLSDSRKMDPAEDTNVYTE 115
DB 76 SP-----SSEMPYVETTLTKTQKMAPETKEPGEVESTNTVLVYGKDI-----VQTA 123
```

```
QY 116 KHSDSLF 122
DB 124 THTENLF 130

RESULT 12
Q90ZY9 PRELIMINARY; PRT; 208 AA.
AC Q90ZY9;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Syndecan-2.
GN Name=sdcc2;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu H., Chou C., Ieu J., Huang C.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Chen S., Ekker S.C.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cell surface proteoglycan (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the syndecan proteoglycan family.
DR EMBL; AF262048; AAK49414.1; -.
DR EMBL; AY091914; AAM14699.1; -.
DR HSP; P31431; 1EJP.
DR ZFIN; ZDB-GENE-021206-3; sdcc2.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008092; P:cytoskeletal protein binding; IEA.
DR Pfam; PF01034; Syndecan; 1.
DR SMART; SM00294; 4.1m; 1.
DR PROSITE; PS00964; SYNDECAN; 1.
KW Glycoprotein; Heparan sulfate; Proteoglycan; Transmembrane.
SQ SEQUENCE 208 AA; 22677 MW; 27A15579219E2B18 CRC64;

Query Match
Best Local Similarity 21.2%; Score 132.5; DB 2; Length 208;
Matches 43; Conservative 24; Mismatches 34; Indels 35; Gaps 8;

QY 5 TSDDKDKMYLDNSSIEBASGYPIDDDDYASAGSGADEVSEPLTTTRPLPKILLTS 63
DB 31 ITD---DIYLE-----EAGSGYPEDDDDFSSGSGAGEVIEDPVTNTLFFVPAKAEPTQ 83

QY 64 AA-----PKVETTLNQNIPAKTQSPETDKKYNLS-----DSERKMDPAEDTNV- 112
DB 84 DSTKDFTPKVTVT-----SQDAPKDSKRRIEAVPVTEDSRR--NPVTSTTSIP 132

QY 113 -----YTKHSDSLPK 123
DB 133 RPPMDPQDVQSENLFQ 148

RESULT 13
Q66I66 PRELIMINARY; PRT; 208 AA.
AC Q66I66;
DT 25-OCT-2004 (TREMELrel. 28, Created)
DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2005, 03:44:30 ; Search time 43 Seconds
(without alignments)
213.531 Million cell updates/sec

Title: US-10-776-989-9
Perfect score: 624
Sequence: 1 RAELTSDDKMDYLNSSIEASGVYPIDDDDYASASGSGADESVESPELTTRPLPKIL 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/iaa/5A COMB.pap:*
2: /cgn2_6/prodata/1/iaa/5B COMB.pap:*
3: /cgn2_6/prodata/1/iaa/6A COMB.pap:*
4: /cgn2_6/prodata/1/iaa/6B COMB.pap:*
5: /cgn2_6/prodata/1/iaa/PCUTS COMB.pap:*
6: /cgn2_6/prodata/1/iaa/backfile1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	100.0	123	1 US-08-078-683A-9	Sequence 9, Appli
2	624	100.0	123	4 US-08-471-970A-9	Sequence 9, Appli
3	624	100.0	123	4 US-09-723-677B-9	Sequence 9, Appli
4	375	60.1	76	4 US-09-621-976-4840	Sequence 4840, Ap
5	205	32.9	43	1 US-08-078-683A-11	Sequence 11, Appl
6	205	32.9	43	4 US-08-471-970A-11	Sequence 11, Appl
7	205	32.9	43	4 US-09-723-677B-11	Sequence 11, Appl
8	180	28.8	43	1 US-08-078-683A-10	Sequence 10, Appl
9	180	28.8	43	4 US-08-471-970A-10	Sequence 10, Appl
10	180	28.8	43	4 US-09-723-677B-10	Sequence 10, Appl
11	102.5	16.4	42	1 US-08-078-683A-12	Sequence 12, Appl
12	102.5	16.4	42	4 US-08-471-970A-12	Sequence 12, Appl
13	102.5	16.4	42	4 US-09-723-677B-12	Sequence 12, Appl
14	96.5	15.5	883	4 US-09-248-796A-18931	Sequence 18931, A
15	88.5	14.2	1416	1 US-08-061-465-4	Sequence 4, Appli
16	87.5	14.0	642	4 US-09-248-796A-15380	Sequence 15380, A
17	87	13.9	196	4 US-09-248-796A-14689	Sequence 14689, A
18	87	13.9	255	4 US-09-370-767-41950	Sequence 41950, A
19	86.5	13.9	700	1 US-07-720-589-2	Sequence 2, Appli
20	86.5	13.9	700	2 US-08-785-190-2	Sequence 2, Appli
21	86.5	13.9	700	3 US-08-235-836C-66	Sequence 66, Appl
22	86.5	13.9	700	5 PCT-US92-05539-2	Sequence 2, Appli
23	86.5	13.8	414	4 US-09-248-796A-19046	Sequence 19046, A
24	85.5	13.7	368	4 US-09-248-796A-19795	Sequence 19795, A
25	85	13.6	746	4 US-09-248-796A-20280	Sequence 20280, A
26	84.5	13.5	708	4 US-08-235-836C-76	Sequence 76, Appl
27	84	13.5	776	2 US-08-700-607-5	Sequence 5, Appli

28	84	13.5	776	4	US-09-949-016-6998	Sequence 6998, Ap
29	83.5	13.4	587	4	US-09-248-796A-18762	Sequence 18762, A
30	82.5	13.2	849	4	US-09-792-024-119	Sequence 119, App
31	82	13.1	1020	4	US-09-538-092-911	Sequence 911, Appli
32	81.5	13.1	1166	4	US-09-200-650B-7	Sequence 7, Appli
33	81	13.0	198	4	US-09-248-796A-27509	Sequence 27509, A
34	81	13.0	333	4	US-09-248-796A-15352	Sequence 15352, A
35	81	13.0	1346	2	US-08-635-121-2	Sequence 2, Appli
36	81	13.0	1346	4	US-08-978-277A-2	Sequence 2, Appli
37	80.5	12.9	241	4	US-09-248-796A-23201	Sequence 23201, A
38	80.5	12.9	748	4	US-09-538-092-541	Sequence 541, App
39	80.5	12.9	952	4	US-09-107-532A-4706	Sequence 4706, Ap
40	80	12.8	300	6	5340934-6	Patent No. 5340934
41	80	12.8	300	6	5340934-6	Patent No. 5340934
42	80	12.8	397	4	US-09-540-236-2128	Sequence 2128, Ap
43	80	12.8	1596	4	US-08-978-277A-4	Sequence 4, Appli
44	79	12.7	687	4	US-09-248-796A-23026	Sequence 23026, A
45	79	12.7	4019	4	US-09-854-133-425	Sequence 425, App

ALIGNMENTS

RESULT 1
US-08-078-683A-9
; Sequence 9, Application US/08078683A
; Patent No. 5486599
; GENERAL INFORMATION:
; APPLICANT: Saunders, Scott
; APPLICANT: Bernfield, Merton
; APPLICANT: Kato, Masato
; TITLE OF INVENTION: Construction and Use of Synthetic
; TITLE OF INVENTION: Constructs Encoding Syndecan
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/078,683A
; FILING DATE: 17-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CME-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-078-683A-9

Query Match 100.0%; Score 624; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.6e-56;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RAELTSDDKMDYLNSSIEASGVYPIDDDDYASASGSGADESVESPELTTRPLPKIL 60
DB 1 RAELTSDDKMDYLNSSIEASGVYPIDDDDYASASGSGADESVESPELTTRPLPKIL 60

QY 61 LTSAPKVTTLNIONKIPAKTSPEETDKKVNLSDSERKMDPAEEDTNYVTEKHS 120
 Db 61 LTSAPKVTTLNIONKIPAKTSPEETDKKVNLSDSERKMDPAEEDTNYVTEKHS 120
 QY 121 LFK 123
 Db 121 LFK 123

RESULT 2

US-08-471-970A-9
 ; Sequence 9, Application US/08471970A
 ; Patent No. 6531295
 ; GENERAL INFORMATION:
 ; APPLICANT: Saunders, Scott
 ; APPLICANT: Bernfield, Merton
 ; APPLICANT: Kato, Masato
 ; TITLE OF INVENTION: Construction and Use of Synthetic
 ; CONSTRUCTS Encoding Syndecan
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII (text)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/471,970A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/078,683
 ; FILING DATE: 17-JUN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kara, Catherine J.
 ; REGISTRATION NUMBER: F-41,106
 ; REFERENCE/DOCKET NUMBER: CME-062DV
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 227-7400
 ; TELEFAX: (617) 227-5941
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 123 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 ; US-08-471-970A-9

Query Match 100.0%; Score 624; DB 4; Length 123;
 Best Local Similarity 100.0%; Pred. No. 3.6e-56;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RAE L T S D K D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 60
 Db 1 RAE L T S D K D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 60
 QY 61 L T S A A P K V E T T L N I O N K I P A O T K S P E E T D K K V N L S D S E R K M D P A E E D T N Y V T E K H S D S 120
 Db 61 L T S A A P K V E T T L N I O N K I P A O T K S P E E T D K K V N L S D S E R K M D P A E E D T N Y V T E K H S D S 120
 QY 121 LFK 123
 Db 121 LFK 123

RESULT 3

US-09-723-677B-9
 ; Sequence 9, Application US/09723677B
 ; Patent No. 669968
 ; GENERAL INFORMATION:
 ; APPLICANT: SAUNDERS, SCOTT
 ; APPLICANT: BERNFIELD, MERTON
 ; APPLICANT: KATO, MASATO
 ; TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN
 ; FILE REFERENCE: 101353-151
 ; CURRENT APPLICATION NUMBER: US/09/723,677B
 ; CURRENT FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 08/471,970
 ; PRIOR FILING DATE: 1995-06-06
 ; PRIOR APPLICATION NUMBER: 08/078,683
 ; PRIOR FILING DATE: 1993-06-17
 ; PRIOR APPLICATION NUMBER: 07/856,869
 ; PRIOR FILING DATE: 1992-03-24
 ; PRIOR APPLICATION NUMBER: 07/757,654
 ; PRIOR FILING DATE: 1991-09-06
 ; PRIOR APPLICATION NUMBER: 07/746,797
 ; PRIOR FILING DATE: 1991-08-12
 ; PRIOR APPLICATION NUMBER: 07/331,585
 ; PRIOR FILING DATE: 1989-03-29
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 123
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 ; US-09-723-677B-9

Query Match 100.0%; Score 624; DB 4; Length 123;
 Best Local Similarity 100.0%; Pred. No. 3.6e-56;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RAE L T S D K D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 60
 Db 1 RAE L T S D K D K M Y L D N S S I E E A S G V Y P I D D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 60
 QY 61 L T S A A P K V E T T L N I O N K I P A O T K S P E E T D K K V N L S D S E R K M D P A E E D T N Y V T E K H S D S 120
 Db 61 L T S A A P K V E T T L N I O N K I P A O T K S P E E T D K K V N L S D S E R K M D P A E E D T N Y V T E K H S D S 120
 QY 121 LFK 123
 Db 121 LFK 123

RESULT 4

US-09-621-976-4840
 ; Sequence 4840, Application US/09621976
 ; Patent No. 6639063
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Giordano, J.Y.
 ; APPLICANT: Jobert, S.
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET.054PR2
 ; CURRENT APPLICATION NUMBER: US/09/621,976
 ; CURRENT FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 19335
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 4840
 ; LENGTH: 76
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-621-976-4840

Query Match 60.1%; Score 375; DB 4; Length 76;
 Best Local Similarity 97.4%; Pred. No. 4.4e-31;
 Matches 74; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 MYLNDSSIEASGVYPIDDDDYASASGSGADEDVESPELTTRPLPKILLTSAAPKVETT 71
DB 1 MYLNDSSIEASGVYPIDDDDYASASGSGADEDVESPELTTRPLPKILLTSAAPKVETT 60
QY 72 TLNIONKIPAOQKSPE 87
DB 61 TLNIONKIPAOQKSPE 76

RESULT 5
US-08-078-683A-11
; Sequence 11, Application US/08078683A
; Patent No. 5486599
; GENERAL INFORMATION:
; APPLICANT: Saunders, Scott
; APPLICANT: Bernfield, Merton
; APPLICANT: Kato, Masato
; TITLE OF INVENTION: Construction and Use of Synthetic
; TITLE OF INVENTION: Constructs Encoding Syndecan
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/078,683A
; FILING DATE: 17-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CME-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-078-683A-11

Query Match 32.9%; Score 205; DB 1; Length 43;
Best Local Similarity 90.7%; Pred. No. 4.4e-14;
Matches 39; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 11 DMVLNDSIEEASGVYPIDDDDYASASGSGADEDVESPELTTR 53
DB 1 DMVLNDSIEEASGVYPIDDDDYSSASGSGADEDIESPVLTT 43
RESULT 6
US-08-471-970A-11
; Sequence 11, Application US/08471970A
; Patent No. 6531295
; GENERAL INFORMATION:
; APPLICANT: Saunders, Scott
; APPLICANT: Bernfield, Merton
; APPLICANT: Kato, Masato
; TITLE OF INVENTION: Construction and Use of Synthetic
; TITLE OF INVENTION: Constructs Encoding Syndecan
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/078,683A
; FILING DATE: 17-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CME-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-078-683A-11

Query Match 32.9%; Score 205; DB 1; Length 43;
Best Local Similarity 90.7%; Pred. No. 4.4e-14;
Matches 39; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 11 DMVLNDSIEEASGVYPIDDDDYASASGSGADEDVESPELTTR 53
DB 1 DMVLNDSIEEASGVYPIDDDDYSSASGSGADEDIESPVLTT 43

RESULT 6
US-08-471-970A-11
; Sequence 11, Application US/08471970A
; Patent No. 6531295
; GENERAL INFORMATION:
; APPLICANT: Saunders, Scott
; APPLICANT: Bernfield, Merton
; APPLICANT: Kato, Masato
; TITLE OF INVENTION: Construction and Use of Synthetic
; TITLE OF INVENTION: Constructs Encoding Syndecan
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,970A
; FILING DATE: 2000-11-28
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: P-41,106
; REFERENCE/DOCKET NUMBER: CME-062DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-471-970A-11

; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,970A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,683
; FILING DATE: 17-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: P-41,106
; REFERENCE/DOCKET NUMBER: CME-062DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-471-970A-11

Query Match 32.9%; Score 205; DB 4; Length 43;
Best Local Similarity 90.7%; Pred. No. 4.4e-14;
Matches 39; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 11 DMVLNDSIEEASGVYPIDDDDYASASGSGADEDVESPELTTR 53
DB 1 DMVLNDSIEEASGVYPIDDDDYSSASGSGADEDIESPVLTT 43
RESULT 7
US-09-723-677B-11
; Sequence 11, Application US/09723677B
; Patent No. 6699968
; GENERAL INFORMATION:
; APPLICANT: SAUNDERS, SCOTT
; APPLICANT: BERNFIELD, MERTON
; APPLICANT: KATO, MASATO
; TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN
; FILE REFERENCE: 101353-151
; CURRENT APPLICATION NUMBER: US/09/723,677B
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 08/471,970
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/078,683
; PRIOR FILING DATE: 1993-06-17
; PRIOR APPLICATION NUMBER: 07/856,869
; PRIOR FILING DATE: 1992-03-24
; PRIOR APPLICATION NUMBER: 07/757,654
; PRIOR FILING DATE: 1991-09-06
; PRIOR APPLICATION NUMBER: 07/746,797
; PRIOR FILING DATE: 1991-08-12
; PRIOR APPLICATION NUMBER: 07/331,585
; PRIOR FILING DATE: 1989-03-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 43
; TYPE: PRT
; ORGANISM: MUS SP

Query Match 32.9%; Score 205; DB 4; Length 43;
Best Local Similarity 90.7%; Pred. No. 4.4e-14;
Matches 39; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 11 DMVLNDSIEEASGVYPIDDDDYASASGSGADEDVESPELTTR 53
DB 1 DMVLNDSIEEASGVYPIDDDDYSSASGSGADEDIESPVLTT 43
RESULT 7
US-09-723-677B-11
; Sequence 11, Application US/09723677B
; Patent No. 6699968
; GENERAL INFORMATION:
; APPLICANT: SAUNDERS, SCOTT
; APPLICANT: BERNFIELD, MERTON
; APPLICANT: KATO, MASATO
; TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN
; FILE REFERENCE: 101353-151
; CURRENT APPLICATION NUMBER: US/09/723,677B
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 08/471,970
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/078,683
; PRIOR FILING DATE: 1993-06-17
; PRIOR APPLICATION NUMBER: 07/856,869
; PRIOR FILING DATE: 1992-03-24
; PRIOR APPLICATION NUMBER: 07/757,654
; PRIOR FILING DATE: 1991-09-06
; PRIOR APPLICATION NUMBER: 07/746,797
; PRIOR FILING DATE: 1991-08-12
; PRIOR APPLICATION NUMBER: 07/331,585
; PRIOR FILING DATE: 1989-03-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 43
; TYPE: PRT
; ORGANISM: MUS SP

Query Match 32.9%; Score 205; DB 4; Length 43;
Best Local Similarity 90.7%; Pred. No. 4.4e-14;
Matches 39; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 11 DMVLNDSIEEASGVYPIDDDDYASASGSGADEDVESPELTTR 53
DB 1 DMVLNDSIEEASGVYPIDDDDYSSASGSGADEDIESPVLTT 43
RESULT 7
US-09-723-677B-11
; Sequence 11, Application US/09723677B
; Patent No. 6699968
; GENERAL INFORMATION:
; APPLICANT: SAUNDERS, SCOTT
; APPLICANT: BERNFIELD, MERTON
; APPLICANT: KATO, MASATO
; TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN
; FILE REFERENCE: 101353-151
; CURRENT APPLICATION NUMBER: US/09/723,677B
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 08/471,970
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/078,683
; PRIOR FILING DATE: 1993-06-17
; PRIOR APPLICATION NUMBER: 07/856,869
; PRIOR FILING DATE: 1992-03-24
; PRIOR APPLICATION NUMBER: 07/757,654
; PRIOR FILING DATE: 1991-09-06
; PRIOR APPLICATION NUMBER: 07/746,797
; PRIOR FILING DATE: 1991-08-12
; PRIOR APPLICATION NUMBER: 07/331,585
; PRIOR FILING DATE: 1989-03-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 43
; TYPE: PRT
; ORGANISM: MUS SP


```
; TYPE: PRT
; ORGANISM: RATTUS RATTUS
US-09-723-677B-10

Query Match      28.8%; Score 180; DB 4; Length 43;
Best Local Similarity 81.4%; Pred. No. 1.5e-11;
Matches 35; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 11 DMVLDNSSIEEASGVYPIDDDDYASAGSGADEVESPGLTT 53
Db 1 DMVLDSSIEEASGLYPIDDDDYSSASGSGAYEDKGPDLTTS 43

RESULT 11
US-08-078-683A-12
; Sequence 12, Application US/08078683A
; Patent No. 5486599
; GENERAL INFORMATION:
; APPLICANT: Saunders, Scott
; APPLICANT: Bernfield, Merton
; APPLICANT: Kato, Masato
; TITLE OF INVENTION: Construction and Use of Synthetic
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/078,683A
; FILING DATE: 17-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CME-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-078-683A-12

Query Match      16.4%; Score 102.5; DB 1; Length 42;
Best Local Similarity 50.0%; Pred. No. 0.0012;
Matches 22; Conservative 9; Mismatches 6; Indels 7; Gaps 2;

QY 13 YLDNSSIEEASGVYPIDDDDYASAGSG----ADEVESPGLTT 52
Db 1 YIDST---ESSGNYPVDDDDYSSGSGIPARGDDEDENVLT 41

RESULT 12
US-08-471-970A-12
; Sequence 12, Application US/08471970A
; Patent No. 6531295
; GENERAL INFORMATION:
; APPLICANT: Saunders, Scott
; APPLICANT: Bernfield, Merton
; APPLICANT: Kato, Masato

Query Match      16.4%; Score 102.5; DB 1; Length 42;
Best Local Similarity 50.0%; Pred. No. 0.0012;
Matches 22; Conservative 9; Mismatches 6; Indels 7; Gaps 2;

QY 13 YLDNSSIEEASGVYPIDDDDYASAGSG----ADEVESPGLTT 52
Db 1 YIDST---ESSGNYPVDDDDYSSGSGIPARGDDEDENVLT 41

RESULT 13
US-09-723-677B-12
; Sequence 12, Application US/09723677B
; Patent No. 6699968
; GENERAL INFORMATION:
; APPLICANT: SAUNDERS, SCOTT
; APPLICANT: BERNFIELD, MERTON
; APPLICANT: KATO, MASATO
; TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN
; FILE REFERENCE: 101353-151
; CURRENT APPLICATION NUMBER: US/09/723,677B
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 08/471,970
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/078,683
; PRIOR FILING DATE: 1993-06-17
; PRIOR APPLICATION NUMBER: 07/856,869
; PRIOR FILING DATE: 1992-03-24
; PRIOR APPLICATION NUMBER: 07/757,654
; PRIOR FILING DATE: 1991-09-06
; PRIOR APPLICATION NUMBER: 07/746,797
; PRIOR FILING DATE: 1991-08-12
; PRIOR APPLICATION NUMBER: 07/331,585
; PRIOR FILING DATE: 1989-03-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 12
; LENGTH: 42
; TYPE: PRT
; ORGANISM: RANA SP
US-09-723-677B-12

Query Match      16.4%; Score 102.5; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 0.0012;
Matches 22; Conservative 9; Mismatches 6; Indels 7; Gaps 2;

QY 13 YLDSIEEASGVPIDDDDYASAGSG---ADEVDVSPELTT 52
Db 1 YIDST---ESSGNYPVDDDDYSSGSGGIPARGDDEENVLIT 41

RESULT 14
US-09-248-796A-18931
; Sequence 18931, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18931
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18931

Query Match      15.5%; Score 96.5; DB 4; Length 883;
Best Local Similarity 27.8%; Pred. No. 0.27;
Matches 32; Conservative 17; Mismatches 37; Indels 29; Gaps 6;

QY 29 DDDYASAGSGADEVSPELTTTTPKILLTSAAPKVETTTLNQN----- 77
Db 466 DDDDESHSQSDEDEDTASPLTPVLTMRKRSSTIT-SIEDDIELEREIKK 524

QY 78 ---KIP-----AQTKSP---EETDKVNLSDSERKMD---PABED-TNYYTE 115
Db 525 QKVKVPAAIEAIEAPSSPEEGEEREKEVEIKQAEAEVDIKFOPTESPTVYPE 579

RESULT 15
US-08-061-465-4
; Sequence 4, Application US/08061465
; Patent No. 5625049
; GENERAL INFORMATION:
; APPLICANT: Monroe, Stephan S.
; APPLICANT: Glass, Roger I.
; APPLICANT: Koopmans, Marion
; APPLICANT: Jiang, Baoming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING HUMAN ASTROVIRUS
; TITLE OF INVENTION: SEROTYPE II AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: 127 Peachtree Street, N.E.
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/061,465
; FILING DATE: 19930512
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.069
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1416 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human Astrovirus
; STRAIN: Serotype 2
US-08-061-465-4

Query Match      14.2%; Score 88.5; DB 1; Length 1416;
Best Local Similarity 27.4%; Pred. No. 3.4;
Matches 34; Conservative 17; Mismatches 44; Indels 29; Gaps 6;

QY 1 RAELTSDKDKMYLD--NSSIEEASGVPIDDDDYASAGSG---ADEDVE----- 46
Db 694 RELLEKGLDRETFLDLIDRIIGERSGYDDDDYDDEDDGWMVGDVDFDYTEVIN 753

QY 47 -----SPELTTRPLPKILLTSAAPKVETTTLNQNIPAOJKSPRETDKEKVNLSDSR 101
Db 754 DQAKTPAPRTTKPKP-----CPEFETETQPLDLSQK---KEKQPEH---EQQVVKSTK 803

QY 102 KMDP 105
Db 804 KNEP 807

Search completed: March 23, 2005, 04:15:19
Job time : 44 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2005, 03:33:40 ; Search time 1350 Seconds
(without alignments)
30.167 Million cell updates/sec

Title: US-10-776-989-9
Perfect score: 624
Sequence: 1 RAEITSDKDKOMLYDNSSIE.....DPAEDTNYVTKHSDSLFK 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	Length	DB ID	Description
1	597	95.7	340	15	US-10-352-839-3	Sequence 3, Appli
2	593	95.0	201	17	US-10-347-022-5	Sequence 5, Appli
3	593	95.0	201	17	US-10-866-589-5	Sequence 5, Appli
4	445.5	71.4	202	15	US-10-347-022-3	Sequence 3, Appli
5	445.5	71.4	202	17	US-10-866-589-3	Sequence 3, Appli
6	427	68.4	201	15	US-10-347-022-4	Sequence 4, Appli
7	427	68.4	201	17	US-10-866-589-4	Sequence 4, Appli
8	427	68.4	211	14	US-10-149-326-4	Sequence 4, Appli
9	187.5	30.0	190	15	US-10-347-022-6	Sequence 6, Appli
10	187.5	30.0	190	17	US-10-866-589-6	Sequence 6, Appli
11	132.5	21.2	208	15	US-10-347-022-2	Sequence 2, Appli
12	132.5	21.2	208	17	US-10-866-589-2	Sequence 2, Appli
13	90.5	14.5	299	16	US-10-767-701-44989	Sequence 44989, A

14	90	14.4	216	16	US-10-767-701-45435	Sequence 45435, A
15	87.5	14.0	180	16	US-10-767-701-82542	Sequence 82542, A
16	87	13.9	288	15	US-10-369-493-6891	Sequence 6891, Ap
17	86.5	13.9	454	15	US-10-425-114-63299	Sequence 63299, A
18	86.5	13.9	700	15	US-10-369-100-66	Sequence 66, Appl
19	86.5	13.9	857	15	US-10-425-114-60120	Sequence 60120, A
20	86	13.8	1018	16	US-10-437-963-122784	Sequence 122784, A
21	85.5	13.7	212	16	US-10-767-701-51911	Sequence 51911, A
22	85	13.6	1637	17	US-10-470-048B-428	Sequence 428, App
23	84.5	13.5	708	15	US-10-369-100-76	Sequence 76, Appl
24	84.5	13.5	1141	15	US-10-282-122A-70251	Sequence 70251, A
25	84	13.5	178	15	US-10-424-599-164167	Sequence 164167, A
26	84	13.5	428	16	US-10-451-467A-448	Sequence 448, App
27	84	13.5	776	15	US-10-660-946-5	Sequence 5, Appli
28	84	13.5	776	15	US-10-267-502-430	Sequence 430, App
29	84	13.5	1257	15	US-10-369-493-6761	Sequence 6761, Ap
30	84	13.5	2009	15	US-10-297-022-13	Sequence 13, Appl
31	84	13.5	2009	15	US-10-664-422-3	Sequence 3, Appli
32	84	13.5	2009	15	US-10-664-422-4	Sequence 4, Appli
33	84	13.5	2009	15	US-10-664-422-3	Sequence 3, Appli
34	84	13.5	2009	15	US-10-664-423-4	Sequence 10, Appl
35	84	13.5	2009	16	US-10-451-126A-10	Sequence 10, Appl
36	83.5	13.4	644	15	US-10-094-749-2667	Sequence 2667, Ap
37	83	13.3	208	16	US-10-788-792-145	Sequence 145, App
38	83	13.3	982	14	US-10-205-823-335	Sequence 335, App
39	83	13.3	1021	9	US-09-815-242-5471	Sequence 5471, Ap
40	83	13.3	1021	9	US-09-815-242-12544	Sequence 12544, A
41	83	13.3	1659	9	US-09-801-368-118	Sequence 118, App
42	82.5	13.2	849	14	US-10-032-585-7026	Sequence 7026, Ap
43	82.5	13.2	4723	15	US-10-359-012-8	Sequence 8, Appli
44	82	13.1	231	15	US-10-424-599-181160	Sequence 181160, A
45	82	13.1	617	9	US-09-864-761-36182	Sequence 36182, A

ALIGNMENTS

RESULT 1

US-10-352-839-3
; Sequence 3, Application US/10352839
; Publication No. US20040013653A1
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Volk, Rudiger
; Horowitz, Arle
; TITLE OF INVENTION: Stimulation of angiogenesis
; via enhanced endothelial expression of syndecan-4
; core proteins
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Microsoft Word version 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/352,839
; FILING DATE: 28-Jan-2003
; CLASSIFICATION: Unknown
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/145,916C
; FILING DATE: 02-Sep-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: BIS-039
; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-352-839-3

Query Match          95.7%; Score 597; DB 15; Length 340;
Best Local Similarity 97.6%; Pred. No. 1e-46;
Matches 120; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 RAE L T S D K D K M Y L D N S S I E E A S G V P I D D D D Y A S A G S G A D E D V E S P E L T T R P L P K I L 60
Db 217 R A E L T S - - D K M Y L D N S S I E E A S G V P I D D D D Y A S A G S G A D E D V E S P E L T T R P L P K I L 274

QY 61 L T S A A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D S 120
Db 275 L T S A A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D S 334

QY 121 L F K 123
Db 335 L F K 337

RESULT 2
US-10-347-022-5
; Sequence 5, Application US/10347022
; Publication No. US20030225018A1
; GENERAL INFORMATION:
; APPLICANT: Stephen C. Ekker
; TITLE OF INVENTION: Syndecans and Angiogenesis
; FILE REFERENCE: 09531-102001
; CURRENT APPLICATION NUMBER: US/10/347,022
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/349,939
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-347-022-5

Query Match          95.0%; Score 593; DB 15; Length 201;
Best Local Similarity 96.7%; Pred. No. 1.2e-46;
Matches 119; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 RAE L T S D K D K M Y L D N S S I E E A S G V P I D D D D Y A S A G S G A D E D V E S P E L T T R P L P K I L 60
Db 217 R A E L T S - - D K M Y L D N S S I E E A S G V P I D D D D Y A S A G S G A D E D V E S P E L T T R P L P K I L 274

QY 61 L T S A A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D S 120
Db 275 L T S A A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D S 334

QY 121 L F K 123
Db 335 L F K 337

RESULT 3
US-10-866-589-5
; Sequence 5, Application US/10866589
; Publication No. US20050037962A1
; GENERAL INFORMATION:
; APPLICANT: Ekker, Stephen C.
; TITLE OF INVENTION: Syndecans and Angiogenesis
```

```
; FILE REFERENCE: 09531-102002
; CURRENT APPLICATION NUMBER: US/10/866,589
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: 10/347,022
; PRIOR FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/349,939
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-866-589-5

Query Match          95.0%; Score 593; DB 17; Length 201;
Best Local Similarity 96.7%; Pred. No. 1.2e-46;
Matches 119; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 RAE L T S D K D K M Y L D N S S I E E A S G V P I D D D D Y A S A G S G A D E D V E S P E L T T R P L P K I L 60
Db 21 R A E L T S - - D K M Y L D N S S I E E A S G V P I D D D D Y A S A G S G A D E D V E S P E L T T R P L P K I L 78

QY 61 L T S A A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D S 120
Db 79 L T S A A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D S 138

QY 121 L F K 123
Db 139 L F K 141

RESULT 4
US-10-347-022-3
; Sequence 3, Application US/10347022
; Publication No. US20030225018A1
; GENERAL INFORMATION:
; APPLICANT: Stephen C. Ekker
; TITLE OF INVENTION: Syndecans and Angiogenesis
; FILE REFERENCE: 09531-102001
; CURRENT APPLICATION NUMBER: US/10/347,022
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/349,939
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-347-022-3

Query Match          71.4%; Score 445.5; DB 15; Length 202;
Best Local Similarity 72.6%; Pred. No. 4.5e-33;
Matches 90; Conservative 18; Mismatches 13; Indels 3; Gaps 2;

QY 1 RAE L T S D K D K M Y L D N S S I E E A S G V P I D D D D Y A S A G S G A D E D V E S P E L T T R P L P K I L 60
Db 21 R E L T S - - D K M Y L D N S S I E E A S G V P I D D D D Y A S A G S G A D E D V E S P L T T S Q L I P I P 78

QY 61 L T S A - A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D 119
Db 79 L T S A S S P K V E T T L N T Q S I T P A Q T S P E E T D K E E V D I S E A E K L G P A I K S T D V Y T E K H S D 138

QY 120 S L F K 123
Db 139 N L F K 142

RESULT 5
US-10-866-589-3
; Sequence 3, Application US/10866589
```

```
Publication No. US20050037962A1
GENERAL INFORMATION:
APPLICANT: Ekker, Stephen C.
APPLICANT: Chen, Eleanor Y.
TITLE OF INVENTION: Syndecans and Angiogenesis
FILE REFERENCE: 09531-102002
CURRENT APPLICATION NUMBER: US/10/866,589
CURRENT FILING DATE: 2004-06-10
PRIOR APPLICATION NUMBER: 10/347,022
PRIOR FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: 60/349,939
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 202
TYPE: PRT
ORGANISM: Mus musculus
US-10-866-589-3

Query Match      71.4%; Score 445.5; DB 17; Length 202;
Best Local Similarity 72.6%; Pred. No. 4.5e-33;
Matches 90; Conservative 18; Mismatches 13; Indels 3; Gaps 2;

QY 1 RAE L S D K D K M Y L D N S S I E E A S G V Y P I D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 60
DB 21 R E L T S - - D K M Y L D N S S I E E A S G V Y P I D D D Y S S A S G S G A D E D I E S P L T T S Q L I P R I S 78

QY 61 L T S A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D 119
DB 79 L T S A S P K V E T L T Q S I T P A Q T E S P E E T D K E E V D I S E A E K L G P A I K S T D V Y T E K H S D 138

QY 120 S L F K 123
DB 139 N L F K 142

RESULT 6
US-10-347-022-4
Sequence 4, Application US/10347022
Publication No. US20030225018A1
GENERAL INFORMATION:
APPLICANT: Stephen C. Ekker
APPLICANT: Eleanor Y. Chen
TITLE OF INVENTION: Syndecans and Angiogenesis
FILE REFERENCE: 09531-102001
CURRENT APPLICATION NUMBER: US/10/347,022
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: 60/349,939
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 201
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-347-022-4

Query Match      68.4%; Score 427; DB 15; Length 201;
Best Local Similarity 69.1%; Pred. No. 2.3e-31;
Matches 85; Conservative 19; Mismatches 17; Indels 2; Gaps 1;

QY 1 RAE L S D K D K M Y L D N S S I E E A S G V Y P I D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 60
DB 21 RAE L T S - - D K M Y L D S S I E E A S G L Y P I D D D Y S S A S G S G A Y E D K G S P L T T S Q L I P R I S 78

QY 61 L T S A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D 120
DB 79 L T S A A P E V E T M L T Q S I T P T Q T E S P E E T D K K E F E I S E A E E K Q D P A V K S T D V Y T E K H S D 138

QY 121 L F K 123
DB 139 L F K 141
```

```
RESULT 7
US-10-866-589-4
Sequence 4, Application US/10866589
Publication No. US20050037962A1
GENERAL INFORMATION:
APPLICANT: Ekker, Stephen C.
APPLICANT: Chen, Eleanor Y.
TITLE OF INVENTION: Syndecans and Angiogenesis
FILE REFERENCE: 09531-102002
CURRENT APPLICATION NUMBER: US/10/866,589
CURRENT FILING DATE: 2004-06-10
PRIOR APPLICATION NUMBER: 10/347,022
PRIOR FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: 60/349,939
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 201
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-866-589-4

Query Match      68.4%; Score 427; DB 17; Length 201;
Best Local Similarity 69.1%; Pred. No. 2.3e-31;
Matches 85; Conservative 19; Mismatches 17; Indels 2; Gaps 1;

QY 1 RAE L S D K D K M Y L D N S S I E E A S G V Y P I D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 60
DB 21 RAE L T S - - D K M Y L D S S I E E A S G L Y P I D D D Y S S A S G S G A Y E D K G S P L T T S Q L I P R I S 78

QY 61 L T S A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D 120
DB 79 L T S A A P E V E T M L T Q S I T P T Q T E S P E E T D K K E F E I S E A E E K Q D P A V K S T D V Y T E K H S D 138

QY 121 L F K 123
DB 139 L F K 141

RESULT 8
US-10-149-326-4
Sequence 4, Application US/10149326
Publication No. US20030100492A1
GENERAL INFORMATION:
APPLICANT: Yavon, Avner
TITLE OF INVENTION: PROTEOGLYCAN AND PHARMACEUTICAL COMPOSITIONS COMPRISING THEM
FILE REFERENCE: 01/22063
CURRENT APPLICATION NUMBER: US/10/149,326
CURRENT FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: IL 133318
PRIOR FILING DATE: 1999-12-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 211
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-149-326-4

Query Match      68.4%; Score 427; DB 14; Length 211;
Best Local Similarity 69.1%; Pred. No. 2.4e-31;
Matches 85; Conservative 19; Mismatches 17; Indels 2; Gaps 1;

QY 1 RAE L S D K D K M Y L D N S S I E E A S G V Y P I D D D Y A S A S G S G A D E D V E S P E L T T R P L P K I L 60
DB 31 RAE L T S - - D K M Y L D S S I E E A S G L Y P I D D D Y S S A S G S G A Y E D K G S P L T T S Q L I P R I S 88

QY 61 L T S A P K V E T T L N I Q N K I P A Q T K S P E E T D K E K V N L S D S E R K M D P A E E D T N V Y T E K H S D 120
DB 89 L T S A A P E V E T M L T Q S I T P T Q T E S P E E T D K K E F E I S E A E E K Q D P A V K S T D V Y T E K H S D 148
```

```
QY 121 LFK 123
Db 149 LFK 151

RESULT 9
US-10-347-022-6
; Sequence 6, Application US/10347022
; Publication No. US20030225018A1
; GENERAL INFORMATION:
; APPLICANT: Stephen C. Ekker
; APPLICANT: Eleanor Y. Chen
; TITLE OF INVENTION: Syndecans and Angiogenesis
; FILE REFERENCE: 09531-102001
; CURRENT APPLICATION NUMBER: US/10/347,022
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/349,939
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-347-022-6

Query Match 30.0%; Score 187.5; DB 15; Length 190;
Best Local Similarity 37.0%; Pred. No. 2.3e-09;
Matches 47; Conservative 23; Mismatches 34; Indels 23; Gaps 6;

QY 3 ELTSDKDKMYLDNNSIEASGVYPIDDDYASASGGA---DEDVESPELTTRPL--- 56
Db 19 ETWQAQDRDLYIDST---ESSGNYPVDDDDYSSGSGGIPAHDDDDNVLTTVQTLISS 75
QY 57 PKILLTSAAPKVETTTLNQKIPACTKSPETDKKVNLSDSERKMDPAEDTN-VYTE 115
Db 76 P-----SSEMPYVDVTTTLTKTQTKWAPETKPGVESTNTVL-----VHENKNIQTA 122
QY 116 KHSDSL 122
Db 123 THTENLF 129

RESULT 10
US-10-866-589-6
; Sequence 6, Application US/10866589
; Publication No. US20050037962A1
; GENERAL INFORMATION:
; APPLICANT: Ekker, Stephen C.
; APPLICANT: Chen, Eleanor Y.
; TITLE OF INVENTION: Syndecans and Angiogenesis
; FILE REFERENCE: 09531-102002
; CURRENT APPLICATION NUMBER: US/10/866,589
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: 10/347,022
; PRIOR FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/349,939
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-866-589-6

Query Match 30.0%; Score 187.5; DB 17; Length 190;
Best Local Similarity 37.0%; Pred. No. 2.3e-09;
Matches 47; Conservative 23; Mismatches 34; Indels 23; Gaps 6;

QY 3 ELTSDKDKMYLDNNSIEASGVYPIDDDYASASGGA---DEDVESPELTTRPL--- 56
Db 19 ETWQAQDRDLYIDST---ESSGNYPVDDDDYSSGSGGIPAHDDDDNVLTTVQTLISS 75
QY 57 PKILLTSAAPKVETTTLNQKIPACTKSPETDKKVNLSDSERKMDPAEDTN-VYTE 115
Db 76 P-----SSEMPYVDVTTTLTKTQTKWAPETKPGVESTNTVL-----VHENKNIQTA 122
QY 116 KHSDSL 122
Db 123 THTENLF 129

RESULT 11
US-10-347-022-2
; Sequence 2, Application US/10347022
; Publication No. US20030225018A1
; GENERAL INFORMATION:
; APPLICANT: Stephen C. Ekker
; APPLICANT: Eleanor Y. Chen
; TITLE OF INVENTION: Syndecans and Angiogenesis
; FILE REFERENCE: 09531-102001
; CURRENT APPLICATION NUMBER: US/10/347,022
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/349,939
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-347-022-2

Query Match 21.2%; Score 132.5; DB 15; Length 208;
Best Local Similarity 31.6%; Pred. No. 0.0003;
Matches 43; Conservative 24; Mismatches 34; Indels 35; Gaps 8;

QY 5 TSDKDKMYLDNNSIEASGVYPIDDDYASASGGAEDVESPELTTRPLPKILLTS 63
Db 31 TTD---DLYLE-----EAGSGYPPEDDDDFSSGSGSGAGEVIEDPVTNTLFFVPKRAEPTQ 83
QY 64 AA-----PKVETTLNQNIPACTKSPETDKKVNLS-----DSERKMDPAEDTNV- 112
Db 84 DSTKDTFTPKVETVT-----SQDAPKDSKKRIEAVPVVTEDSRR--NPVTTSTTIP 132
QY 113 -----YTEKHSDSLFK 123
Db 133 RPPMDPQDVQSENLFQ 148

RESULT 12
US-10-866-589-2
; Sequence 2, Application US/10866589
; Publication No. US20050037962A1
; GENERAL INFORMATION:
; APPLICANT: Ekker, Stephen C.
; APPLICANT: Chen, Eleanor Y.
; TITLE OF INVENTION: Syndecans and Angiogenesis
; FILE REFERENCE: 09531-102002
; CURRENT APPLICATION NUMBER: US/10/866,589
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: 10/347,022
; PRIOR FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/349,939
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-866-589-2

Query Match 21.2%; Score 132.5; DB 17; Length 208;
```


THIS PAGE BLANK (USPTO)